Single chain Fv pr Lead binding MAb 1 Heavy chain amino MaE13 heavy chain. Fv (TU27). Homo sa Interleukin-6 spec

AAY55079
AAY55080
AAY55081
AAY55081
AAY55081
AAX55082
AAW01584
AAX33308
AAX34510
AAX34510
AAX55072
ABB98906

Variable region an Variable region an Variable region an Antibody 24-31 hum Murine wild-type a Sequence encoded b Heavy chain of 58.
Variable region an Sequence of the mo Humanised antibody 5H7 single chain a Monoclonal antibod Mouse VH group I (A Variable heavy cha Anti-human FasL an

AAW21937 AAY05267 ABG98318 AAR24722 AAR63118 ABB98908

AAR48617

Antibody 5H7 heavy Sequence of a chim Variable domain of VH domain of antib Monoclonal antibod Monoclonal antibod G28.5 FV protein. BD1-G28.5 fusion g Humanised antibody

ABP58448 AAY95781 AAK64201 AAW00829 AAW19015 AAW19015 AAX95776 AAX95776 AAX95776 AAX967318

Variable heavy sub Antibody 24-31 hum

AAB36828 ABP58447 AAW21935 AAY05265

AAR99875 AAB36827 ALIGNMENTS

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Human, antibody, interleukin-6, receptor, IL-6R, light chain, L, H, heavy chain, variable region, mouse, monoclonal, hybridoma, PM1, plasmid, pPM-k3, pPM-h1.
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/note=_"Signal peptide"
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/note= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR28671 standard; Protein; 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-JP00544
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(first entry)
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19-FEB-1992;
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30-MAR-1993
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Synthetic
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Peptide
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 Murine 5B3 antibod
MAD 1.4 heavy chai
Monoclonal antibod
pUC-RVh-PM1f. Syn
pUC-RVh-PM1f. Syn
Single chain Fv pr
Single chain Fv pr
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Antibody 806 varia
                                                                                        ; Search time 61.7538 Seconds (without alignments) 352.133 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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1 MRVLILLWLFTAFPGILSDV.....LARTTAMDYWGQGTSVTVSS
                                                                                                                                                                                                                                                                  1107863
            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                     1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                               protein search, using sw model
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ABB82796
AAB15672
AAW01144
AAW44169
AAR29012
AAR29014
AAY55075
                                                                                          October 22, 2003, 22:03:25
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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82.7
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Perfect score:
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588
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The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is recognizes an epidermal growth factor receptor (EGFR) epitope which is found in tumourigenic, hyperpoliferative or abnormal cells and not detectable in normal cells. The EGFR epitope is located within the region acid sequence alterations or substitutions. From normal EGFR. (I) is capable of binding the de-7 EGFR at an epitope distinct from the innormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprises the VH and VL cormal wild-type gene. The binding member comprised with the presence of amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation is suspected with (I) under conditions that allow binding the presence of amplified EGFR, from the sample and the antibody, where the corner between the EGFR from the sample and the antibody, where the corner the EGFR to the artibody to occur, and detecting cancer in mammals by detecting the presence or activity of an EGFR with indicates the existence of a tumour or cancer in the mammal. A pharmaceutical comprising and/or treating cancer in mammals, sepecially for treating brain-resident cancers that produce aberrantly expressed EGFR in mammals, sepecially expressed EGFR in mammals, under sequence represents the mammals. And malignant maniglomar, and malignant cancer in mammals. The present sequence represents the mammals and malignant cancer in mammals. The member of mammals and malignant cancer in mammals. The member of mammals and the analyses and malignant cancer in mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRVLILLWLFTAFPGVLSDVQLQESGPSLVKPSQSLSLTCTVTGYSITSDFAWNWIRQFP 60
                                                                                                                                                                             Novel specific binding members, particularly antibodies recognizing epidermal growth factor receptor epitope found only in tumorigenic cells, useful for diagnosing, preventing and treating cancer in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 593.5; DB 24; Length 134;
Pred. No. 1.8e-46;
5; Mismatches 14; Indels 3;
     is C, Scott AM, Renner C, Ritter
Collins P, Cavenee WK, Huang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                             Claim 6; Fig 14B; 123pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.7%;
Best Local Similarity 83.9%;
Matches 115; Conservative 5
       Panousis
Old LJ, Johns TG, Lunglungbluth A, Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-2001 (first entry)
                                                                                                           WPI; 2003-129282/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 AA;
                                                                                                                                   N-PSDB: ABZ23940
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                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
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                                                                                                                                                                                  Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 718; DB 13; Length 137; 100.0%; Pred. No. 8.7e-58; cive 0; Mismatches 0; Indels 0.
                                                            Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody 806 variable heavy chain (VH) region.
                                                         Saldanha JW, Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..18
/note= "signal peptide"
19..134
/note= "mAb 806 VH region"
                                                                                                                                                                                                                                                                                     Disclosure; Page 122-123; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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28-SEP-2001; 2001US-326019P.
21-DEC-2001; 2001US-342258P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 137; Conservative
       (CHUS ) CHUGAI SEIYAKU
                                                       Bendig MM, Jones ST,
                                                                                                           WPI; 1992-398882/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AA;
                                                                                                                                   N-PSDB; AAQ30756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200292771-A2
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ABB82796;

RESULT 2 ABB82796 Peptide Protein

Key

Sequence Query Match

ò 셤 ò 셤 ò g

9

3; Gaps

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61 GNKLERMGYIRYSGYTSYNPSLKSRIFITRDTSQNQFFLHLTSVTTEDTATYYCTRDL-D 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infarction, acute kidney failure, chronic rheumatism, carebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and collifis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myetlome B3U1 (Pax6Apg U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody 1.4 heavy chain against type II phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibodies which inhibit type II phospholipase A2 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
78.3%; Score 562.5; DB 17;
Best Local Similarity 81.0%; Pred. No. 1.2e-43;
Matches 111; Conservative 6; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Yasunaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particularly suitable for preclinical testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Takasaki J,
                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Figure 11; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44169 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   (YAMA ) YAMANOUCHI PHARM CO LTD
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                                                                49..54
/label= CDR 1
69..84
/label= CDR 2
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                                                                                                                                                      117..125
/label= CDR
                                                                                                                                                                                                                                                                                                                                                          94JP-0340006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawauchi Y, Masuho Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-333946/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT40804
                                                                                                                                                                                                                                                                                                              27-DEC-1995;
  Mus musculus
                                                                  Binding-site
                                                                                                          Binding-site
                                                                                                                                                      Binding-site
                                                                                                                                                                                                                        WO9620959-A1
                                                                                                                                                                                                                                                                                                                                                          29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW44169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the heavy chain variable region of 5B3 antibody. The CDNA encoding this sequence was obtained from total RNA extracted from a SB3 hybridoma by RT-PCR. 5B3 is an igg1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a piezoelectric immunoassaying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody, phospholipase, myocardial infarction, aparoreatitis, cerebral infarction, acute kidney failure, colitis, chronic rheumatism, adult respiratory distress syndrome, cardiac shock, treatment, preclinical testing, disease, hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                              Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;
small molecule explosive detection; 2,4,6-trinitrotoluene; TNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAb 1.4 heavy chain, directed against type II phospholipase A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apparatus for detecting small molecules, especially explosives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.9%; Score 588; DB 21; Length 136; 83.8%; Pred. No. 5.8e-46; ive 8; Mismatches 12; Indels ;
                  Murine 5B3 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises a piezoelectric crystal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW01144 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3A; 90pp; English
                                                                                                                                                                                                                                                                                                                                                     (YISS ) YISSUM RES & DEV CO. (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TT--AMDYWGQGTSVT 134
                                                                                                                                                                                                                                                                  25-JAN-2000; 2000WO-IL00048
                                                                                                                                                                                                                                                                                                              99IL-0128212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Willner I, Eshhar Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-524259/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-524259/
N-PSDB; AAA74604.
                                                                                                                                                                          WO200043774-A2.
                                                                                                                                                                                                                                                                                                              25-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1997
                                                                                                                                                                                                                      27-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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9 9

1; Gaps

Indels

g

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g ò

'note= "Leader peptide"

CDR1

50..55 /label=

56..69 /label= FR2

FR1

20..49 /label=

CDR2

/label=

/label= FR3

/label= FR4

Location/Qualifiers

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Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; complemantarity determining region; mouse; monoclonal; hybridoma; plasmid; polymerase chain reaction; amplify.
                                                                                                                                                                                                                                                                                    ,18..127
/label= CDR3
128..1.0
(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-1991;
19-FEB-1992;
                                  DUC-RVh-PM1£
                                                                                                                                                                                                                                                                                                                                                        W09219759-A1
25-MAR-2003
30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                            Peptide
                                                                                                                                                                       Region
                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                             Region
                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                       The present sequence represents the monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention. The present invention of the present invention of the present invention of Kidney disorders (such as a cute renal failure) associated with the administration of cisplatin for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the comprises treatment with a monoclonal antibody witch inhibits the phospholipase A2 of human origin), or with a protein or peptide possessing the same inhibitory activity and containing a part of the possesing the same inhibitory activity and containing a part of the apendor mouse type II phospholipase A2, and has the ability to release type II phospholipase A2, and has the ability to release type II phospholipase A2 bound to a cell membrane. Three specific monoclonal antibodies having these properties which can be used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-529 and FERM BP-529 respectively. The method can be used for cisplatin administration, and therefore allowing more efficient use of this drug as an anticancer agent, e.g. by allowing an increased dosage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNKLERMGYIRYSGYTSYNPSLKSRIFITRDTSQNQFFLHLTSVTTEDTATYYCTRDL-D 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
           Monoclonal antibody, type II phospholipase A2, inhibition, cisplatin, amelioration, kidney disorder, nephrotoxicity, anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                Amelioration of kidney disorders caused by cisplatin administration - by treatment with an antibody inhibiting type II phospholipase A2 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Indels
                                                                                                                                                                                                          Takasaki J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 562.5; DB :
Pred. No. 1.2e-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 38; 74pp; Japanese.
                                                                                                                                                                                                          Masuho Y,
                                                                                                                                                                                 (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.3%;
81.0%;
                                                                                                                       97WO-JP02241
                                                                                                                                             96JP-0247635
96JP-0167286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWYFDVWGAGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.0
Matches 111; Conservative
                                                                                                                                                                                                         Kawauchi Y,
                                                                                                                                                                                                                                 WPI; 1998-076914/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA;
                                                                                                                                                                                                                                              N-PSDB; AAV12261
                                                Unidentified
                                                                                                                      27-JUN-1997;
                                                                       WO9749427-A1
                                                                                                                                              19-SEP-1996;
                                                                                                                                                          27-JUN-1996;
                                                                                                                                                                                                        Hayashi K,
                                                                                               31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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AAR29012
ID AAR2
XX
AC AAR2
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92WO-JP00544

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAR29012-15 are portions of monoclonal antobodies which were encoded by plasmids derived from mouse hybridomas. The DNA encoding complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The mouse hybridoma cells were transformed with the plasmids encoding these genes which caused the secretion of these antibodies from the hybridoma cells. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                    has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                             Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.9%; Score 538; DB 13; Length 138; 75.9%; Pred. No. 2.1e-41; Live 15; Mismatches 17; Indels
                                                                                                                        Tsuchiya M;
                                                                                                                        Sato K,
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138-9; 207pp; Japanese.
                                                                                                                        Saldanha JW,
91JP-0095476.
92JP-0032084.
                                                                          (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                          Jones ST,
                                                                                                                                                                        WPI; 1992-398882/48;
N-PSDB; AAQ31360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 AA;
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AAR29012 standard; Protein; 138 AA.

AAR29012

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64 65

AAR29014 RESULT

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EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM 124
                                                                                                                                                              This sequence represents a single chain FV (ScFV) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein
                                                                                            6 ILFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
                                                                       5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Efficient and selective isolation of a gene encoding membrane protein
                                     Gaps
                                   ö
Length 138;
                                   17; Indels
Query Match 74.9%; Score 538; DB 13; Best Local Similarity 75.9%; Pred. No. 2.1e-41; Matches 101; Conservative 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain Fv protein sequence shPM1(deltaEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 80-82; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                              AAY55075 standard; Protein; 260 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0138652
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|DYWGQGSLVTVSS 138
                                                                                                                                                                                                                     DYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuchiya M, Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-039382/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ40305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9960113-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                    AAY55075;
                                                                                                                                             65
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                                                                                                                                                                                                                                                         126
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                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                 AAY55075
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                                                                                                                                                                                                                                                                                         Human, antibody, interleukin-6; receptor; IL-6R; CDR; PCR;
complemantarity determining region; mouse; monoclonal; hybridoma;
plasmid; polymerase chain reaction; amplify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 142-3; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                          AAR29014 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56..69
/label= FR2
70..85
/label= CDR2
86..117
/label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118.:127
/label=_CDR3
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/label= CDR1
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/label= FR4
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/label= FR1
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 137
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126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                  (updated)
(first entry)
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DYWGQGTSVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-398882/48.
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                                                                                                                                                                                                                                                       DUC-RVh-PM1f-4.
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19-FEB-1992;
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30-MAR-1993
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125
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                                                                                             65 EWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARSLARTTAM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a single chain Fv (ScFv) sequence.

The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein -
                                                           5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
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Length 260;
                        Indels
                          17;
 DB 21;
             5.3e-41
                                                                                                                                                                                                                                                                                                  Single chain Fv protein sequence shPM1-Kappa.
  74.8%; Score 537; DB 275.9%; Pred. No. 5.3e-4.ive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 86-89; 120pp; Japanese.
                                                                                                                                                                                                                            AAY55078 standard; Protein; 367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohtomo T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0138652.
98JP-0279876.
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                                                                                                                                           125 DYWGOGTSVTVSS 137
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126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                         (first entry)
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Query Match
Best Local Similarity 75.9°
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-039382/03.
N-PSDB; AAZ40308.
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                                                                                                                                                                                                                                                                                                                                                                                           WO9960113-A1
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74.8%; Score 537; DB 21; Length 367;

Query Match

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The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TWT) method wherein an epitope recognised by an antibody is carried in a fused
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                                                                                                                                                                                             EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM
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                            Indels
7.8e-41;
ches 17;
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Pred. No. 8.1e-41;
  Pred. No. 7.8e-
5; Mismatches
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75.9%;
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98JP-0279876.
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  Best Local Similarity 75.9%
Matches 101; Conservative
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N-PSDB; AAZ40309.
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Best Local Similarity
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01-OCT-1998;
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1LLWLFTAFPG11LSDVQLQESGPVLVKPSQSLSLTCTVTGYS1TSDHAWSW1RQFPGNKL
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                                                                                                                                                        This sequence represents a single chain FV (ScFV) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective,
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                                           ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM
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  17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain Fv protein sequence shPM1(deltaEL)-BvGS3.
  15; Mismatches
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98JP-0279876.
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101; Conservative
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Best Local Similarity 75.9
Matches 101; Conservative
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N-PSDB; AAZ40312.
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01-OCT-1998;
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The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the CDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene isolation, membrane-bound protein; fusion protein; drug production, antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SCFV.
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6 ILLFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
                                                                            EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLARTTAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single chain Fv protein sequence hPM1-BvGS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 73-78; 120pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY55074 standard; Protein; 546 AA.
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                                                                                                                                                                                                                          125 DYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                               126 DYWGQGSLVTVSS 138
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsuchiya M, Saito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-039382/03.
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6 IILFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL 65
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                                                                                                                                               RESULT 14
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                                                                                                                                                                      This sequence represents a single chain Fv (ScFv) sequence.

The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, the protein is such a technique is efficient and selective.
                      65
                                                                                                                                                                                                                                                                            Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; ScFv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Efficient and selective isolation of a gene encoding membrane protein with low or no antigenic binding activity, for diagnosis, study of, and production of drugs treating abnormal functions of the protein
             6 ILFLVATATGVDSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL
ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                 EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which is different from the prior-art transmembrane trap (TMT) methwherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.8%; Score 537; DB 21; Length 626; 75.9%; Pred. No. 1.4e-40;
                                                                                                                                                                                                                                                         Singl'e chain Fv protein sequence shPM1-kappa-BvGS3.
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                                                                                                                                                                                 AAY55081 standard; Protein; 626
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98JP-0279876
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126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                 (first entry)
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                                                                                               125 DYWGQGTSVTVSS
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N-PSDB; AAZ40316.
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The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a CDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene isolation; membrane-bound protein; fusion protein; drug production; antigen-binding cell; secretable functional protein; antigenic protein; protein isolation; diagnosis; SCFV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Efficient and selective isolation of a gene encoding membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with low or no antigenic binding activity, for diagnosis, study production of drugs treating abnormal functions of the protein
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ilarity 75.9%; Pred. No. 1.4e-40;
Conservative 15; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 111-117; 120pp; Japanese.
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                                                                                                                                                                               126 DYWGOGSLVTVSS 138
                                                                                                                          DYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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01-OCT-1998;
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5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64

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Gaps

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17; Indels

15; Mismatches

Matches 101; Conservative

Best Local Similarity

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                                                    66 EWIGYISYSGITTYNPSLKSRVTWLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                  EWMGYISYSGITTYNPSLKSRISITRDISKNQFFLQLNSVTTGDISTYYCARSLARTTAM 124
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 6 IILFLVATATGVDSQVQLQESGFGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 13D10, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of
                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody, Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide; heavy metal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4%; Score 534; DB 18; Length 119; 85.7%; Pred. No. 4.1e-41; ive 6; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                     Lead binding MAb 13D10 heavy chain variable region.
                                                                                                                                                                                                                      AAW01584 standard; Protein; 119 AA
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                                                                                                     DYWGQGTSVTVSS 137
                                                                                                                                    126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 85.7
Matches 102; Conservative
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N-PSDB; AAT58258.
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05-JUN-1995;
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(c) 1993 - 2003 Compugen Ltd.
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Ig heavy chain - !	Ig heavy chain - h	Ig heavy chain V r	Ig mu heavy chain	Ig heavy chain pre	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain.pre	Ig mu heavy chain	To heavy chain V r					
831511	831512	S13519	S31690	S14486	S09711	S31676	S14487	S54236	S78055	S31586	S30530	S78051	A32456	S54249	513685
N	N	0	N	~	~	7	8	~	~	7	~	7	7	~	r
22	155	147	130	102	146	137	102	141	145	139	123	135	139	143	112
Н															
57.7 1	57.5	56.8	56.7	9.95	56.4	56.3	56.0	55.6	55.1	54.9	54.9	54.9	54.9	54.5	7 A R

## ALIGNMENTS

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R;Near, R.I.; Haber, E. Mander, PL0100; MUID:89238344; PMID:2497340
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M27660; NID:g341745; PIDN:AAA58746.1; PID:g609530
A;Experimental source: strain A/J
A;Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GNRLEWMGYITYNGYTTYNPSLKSRFSITRDTSKNQLFLQLSSVTTEDTATYYCARSY-- 118
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                                                 Ig heavy chain precursor V region (40-140) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <8]
F;19-115/Domain: V segment #status predicted <VRE>
F;33-116/Domain: immunoglobulin homology <IMM>
F;117-118/Domain: D segment #status predicted <DRE>
F;119-135/Domain: J segment #status predicted <JRE>
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A; Molecule type: DNA
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RESULT 1
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Ig heavy chain precursor V region - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 23-Jul-1999 C;Accession: S3075; C;Accession: S3075, S.D.; Gilbert, T.; Kindsvogel, W. Nuclaic Acids Res. 15, 5496, 1987 A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

-DYFDYWGQGTTLTVSS 134

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RESULT 2

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A; Reference number: JT0501; MUID:89279149; PMID:2499654
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J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 heavy chain precursor V region (VGAM3-2) - mouse C.Species: Mus musculus (house mouse) C.Species: Basedown: B24672  
R.Winter, E.; Radbruch, A.; Krawinkel, U. EMBO J. 4, 2861-2867, 1985  
A.Reference number: A91022; MUD:86055722; PMID:2998759  
A.Accession: B24672  
A.Accession: B24672  
A.Accession: B24672  
A.Molecule type: DNA A.Residues: 1-134  
A.Molecule type: DNA A.Residues: 1-134  
A.Introns: 15/1  
C.Souperfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin nomology C.Keywords: heterotetramer; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GNKLEWMAYIHYSGNTDENPSLKSRISITRDTSKNOFFLQLNSVTAEDTATYYCARGYGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Aug-1996
C;Accession: JT0508
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                  A,Accession: S30752
A,Molecule type: mRNA
A,Molecules: 1-194 oGRA-
A,Residues: 1-194 oGRA-
A,Cross-references: EMBL:X05878, NID:g52526; PIDN:CAA29302.1; PID:g52527
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin Nom
F;33-116/Domain: immunoglobulin homology oinm>
F;338-149/Domain: C region (C-gamma 2b) (fragment) #status predicted <CRI
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Reference number: S30751; MUID:87260030; PMID:3601683
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                                                                                                                                                                                                                                                 Score 593; DB 2;
Pred. No. 9.1e-45;
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82.5%;
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Best Local Similarity 84.7%;
Matches 116; Conservative
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A,Molecule type: DNA
A,Residues: 1-15,'G',16-137 <RI2>
A,Residues: 1-15,'G',16-137 <RI2>
A,Cross-references: EMBL.X07880; NID:g51760; PIDN:CAA30727.1; PID:g295908
A,Cross-references: EMBL.X07880; NID:g51760; PIDN:CAA30727.1; PID:g295908
R,Jilka, R.L.; Pestka, S.
Proc. Natl. Acad. Sci. U.S.A. 74, 5692-5696, 1977
A,Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he A,Reference number: A93814; MUID:78094475; PMID:414225
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A;Residues: 19-52, R',53-75, BYGB', 80-101,'D',103-106,'ZB',109-122,124-137 <FRA>
R;Hood, L.; Margolles, M.; Givol, D.; Zakut, R.
unpublished results, cited by Padlan, E.A., Davies, D.R., Pecht, I., Givol, D., and Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a mous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the heavy (alpha) chain of
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A; Residues: 1-14, 'H',16-31 <JIL>
A; Residues: 1-14, 'H',16-31 <JIL>
A; Residues: translated mRNA in vitro to obtain the precursor protein
R; Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed Proc. 38, 1839-1845, 1979
A; Title: Structure and function of immunoglobulin genes and precursors.
A; Reference number: A91462; MUID: 79148758; PMID: 428562
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A;Residues: 1, 'X', 3-11, 'X', 14-21 <SCH>
A;Note: the authors translated mMA in vitro to obtain the precursor protein
R;Francis, S.H.; Leslie, R.G.O.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A;Title: Amino-acid sequence of the variable region of the heavy (alpha) chai
A;Reference number: A93787; MUID:74170779; PMID:4524622
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A;Molecule type: mRNA
A;Residues: 1-137 <RIN>
A;Cross-references: GB:M27638; NID:g602706; PIDN:AAA61337.1; PID:g602707
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 543; DB 1; Length 116;
Pred. No. 1.6e-40;
4; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: strain MOPC
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Best Local Similarity 90.5%;
Matches 105; Conservative 4
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acid

9

Gaps

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A;Accession: I28195
A;Molecule type: mRNA
A;Residues: 1-17 < SHB-
A;Cross-references: GB:M19775; NID:g195526; PIDN:AAA38343.1; PID:g195527
A;Note: the authors translated the codon AAC for residue 61 as Thr, and did not translate c;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: 507637
R;Urakov, D.N.; Deev, S.M.; Polyanovsky, O.L.
Nucleic Acids Res. 17, 9481, 1989
A;Title: The structure of the expressible VH gene from a hybridoma producing monoclonal
A;Reference number: 507637; MUID:90067954; PMID:2587273
A;Accession: 507637
A;Molecule type: DNA
                                                                                                                                      Hypervariable region amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S38718
R;Cimanis, A.Y.
Submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Reference number: S38718
A;Reference number: S18718
A;Reference number: Cimanis A;Reference number: S18718
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                          C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: 128195
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <1MM>
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                                                                               R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. B
A;Reference number: A28195; MUID:88153717; PMID:3267217
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 532; DB 2; L
Pred. No. 1.4e-39;
6; Mismatches 9;
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Pred. No. 1.4e-38;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revisio
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Best Local Similarity 84.0%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 74.1%;
al Similarity 85.7%;
102; Conservative
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Best Local Similarity
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              A;Contents: annotation; revision to residue 53
R;Cheadle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.
Mol. Immunol. 29, 21-30, 1992
Mol. Immunol. 29, 21-30, 21-30, 1992
My Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315
A;Reference number: 823599; MUID:92114886; PMID:1731188
A;Accession: 823599
A;Molecule type: mRNA
A;Residues: 19-137 cCHB
A;Cross-references: EMBL:X63972; NID:953532; PIDN:CAA45384.1; PID:9938267
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe A;Introns: 15/1
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(53285

Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: C53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular charactefization of monoclonal anti-steroid antibodies: primary struct and their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-136/Product: Ig heavy chain V region (MOPC 315) #status experimental <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA; protein
A;Molecule type: mRNA; protein
A;Residues: 1-119 <SAM>
A;Cross-references: GB:D12734; NID:g220548; PIDN:BAA02226.1; PID:g220549
A;Cross-reference extracted from NCBI backbone (NCBIN:61297, NCBIP:63302)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V region (anti-haloperidol antibody D) - mouse
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84.9%; Pred. No. 6.6e-40;
ive 6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 538; DB 1;
; Pred. No. 5.1e-40;
15; Mismatches 21
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73.7%;
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Best Local Similarity 73.7%
Matches 101, Conservative
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  A; Reference number: A94484
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78

Gaps

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F;1-18/Domain: signal sequence #status predicted F;19-116/Product: Ig heavy chain V region (M315) F;33-116/Domain: immunoglobulin homology <IMM>
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8
                                                                                               71.0%;
83.6%;
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Best Local Similarity 77.7%;
Matches 94; Conservative
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78.2%;
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Best Local Similarity 78.2
Matches 93; Conservative
                                                                                                                     Similarity
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A;Residues: 1-121 <FIS>
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A; Status: preliminary
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Matches
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A,Reference number: JT0501
A,Reference number: Another not shown
A,Residues: 1-116 <LEV>
A,Residues: 1-116 <LEV>
A,Residues: 1-116 <LEV>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
  PIDN:CAA34714.1; PID:9297543
for residue 112 as Ile, TAC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, E.K.; Scharff, M.D.
ADS Res. Hum. Retroviruses 9, 41-49, 1993
A;Tile: Variable region gene utilization and mutation in a group of neutralizin A;Reference number: Z14285; MUID:93152285; PMID:7678971
A;Accession: T01262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Cype: mRNA
A;Residues: 1-114 <PIR.
A;Cross-references: EMBL:S54194; NID:g264864; PIDN:AAB25246.2; PID:g5705887
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Aug-1996
Accession: JT0509
                                                                                                                                                                                                                                                                                                               1 DVQLQQSGPGLVKPSQSLSHTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISFSGSTSY
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د.
                                                                                                                                                                                       Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                  Aintrons: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                        Indels
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R, Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart,
J. Exp. Med. 169, 2007-2019, 1989
                                                                                                                                                                                         Score 519.5; DB 2;
Pred. No. 2.1e-38;
9; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.1%; Score 517.5; DB 2; Best Local Similarity 83.2%; Pred. No. 2.6e-38; Matches 99; Conservative 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain precursor V region (M315) - mouse
  EMBL:X16740; NID:g52099;
translated the codon TAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TTAMD-----YWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- DGYHFFTYWGQGTLVTVSA 136
                                                                                                                                                                                         Query Match
Best Local Similarity 72.7%;
Matches 104; Conservative
Cross-references:
Note: the authors
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
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Igheavy chain V region (HP25) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Spaces: 29-Aug-1987 #sequence_revision 29-Aug-1987 #sequence_revision 29-Aug-1987 #sequence_revision 25-Aug-1987 #sequence (Species: 30-Species: Musculus (Musculus Musculus Musc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse) .
C;Dacession: 837-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: 837200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: 837200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKVLSLLYLLTAIPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFP
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                                                                                                                                                                                                                                                                                                                                                                                               1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR 116
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                                              <MAT>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                  Length
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#status |
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1.5e-35;
ches 17;
                                                                                                                                                                                             Score 510; DB 1;
Pred. No. 1.2e-37;
8; Mismatches 11;
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Pred. No. 6.1e-35;
6; Mismatches 14,
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Pred. No. 1.5e-
8; Mismatches
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RESULT 15
D33932
Ig wu chain precursor V region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Dates: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-May-1997
C;Accession: D33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1
A;Accession: D33932
A;Accession: D33932
A;Accession: D33932
A;Accession: D33932
A;Reference number: A3932; MUD:89262823; PMID:2499887
A;Molecule type: mRNA
A;Residues: 1-115 cBAC>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                      KESULI 13

S26464

Ig heavy chain V region - mouse

C; Speciess Mus musculus (house mouse)

C; Speciess in S26464

E; Ravaler, J.

S; Ravaler, J.

S; Ravaler, J.

S; Ravaler to the EMBL Data Library, April 1991

A; Reference number: S26459

A; Accession: S26464

A; Reference number: S26459

A; Residues: 1-106 < KAV.

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Superfamily: immunoglobulin homology < IMM.
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  78
                              1 DVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYYWNWIRQFPGNKLEWMGYISYDGSHNY 60
                                                                                                       79 NPSLKSRISITRDISKNOFFLQLNSVITGDISTYYCARSL-----ARTTAMDYWGQGT 131
                                                                                                                                         61 NPSLKNRISITRDISKNQFFLKLNSVTIEDTATYYCARPLYYRYDEEYYYAMDYWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 KPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYNPSLKSRISITR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 66.6%; Score 478.5; DB 2; Length 106; I Similarity 84.1%; Pred. No. 5.9e-35; 90; Conservative 8; Mismatches 8; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISKNOFFLOLNSVITGDISTYYCARSLARTTAMDYWGOGTSVTVSS 137
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Best Local S
Matches 90
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Search completed: October 22, 2003, 22:18:06 Job time: 26.947 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 22, 2003, 22:10:20 ; Search time 14.0114 Seconds (without alignments) 459.817 Million cell updates/sec Run on:

Title: US-09-114-285A-31
Perfect score: 718
Sequence: 1 MRVLILLWLFTAFPGILSDV.....LARTTAMDYWGOGTSVTVSS 137

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	esci	1853	P0182	P18533	P1853	P0182	P0181	P06331	P2095'	P0182	P0182	0182	P0181	P01821	P2095	0181	P0443	P0181	P0181	P0178	P01751	0174	P0175	P0176	P0176	P0181	P0177	~	~	P0178	P0179	P0174	P0181	017
SUMMARIES		MOUSE	NOUSE	MOUSE	MOUSE	MOUSE	MOUSE	HUMAN	XENLA	HUMAN	MOUSE	HUMAN	HUMAN	MOUSE	XENLA				IUMAN	NOUSE	NOUSE	MOUSE	MOUSE	HUMAN	HUMAN	HV2A HUMAN P(	HUMAN	HUMAN	MOUSE	MOUSE	MOUSE	MOUSE	MOUSE	HUMAN
	ID	HV61		HV60_1	HV62	HV47	HV43	HV2I	HV02	HV2G	HV44	_	_		_	_	HV2]	HV2	HV2	HV16	HV07	HV02	HV11	HA3	HV3H	HV2	HV3	HV3G	HV13	HV17	HV15	HV03	HV42	HV3J
	DB							-	Н	٦	1	Н		٦			Н	~	Н	7	Н	Н	-	Н	Н	Н	-	-	Н	Н	7	Н	Н	-
	Length	116	137	116	117	113	144	146	135	117	115	129	121	116	136	119	147	125	120	136	139	140	137	115	122	126	119	. 122	117	117	136	120	117	121
a	Query Match	75.6	74.9	71.0	64.3	•	53.6	52.6	47.1	٠	46.0		•	•	•	•	41.2	•	•			ö	σ.	e.		œ.	œ.	•	•	38.2	•	38.0	37.9	٠
	Score	543	538	510	461.5	450	384.5	377.5	338	337	330	328	323	316	312.5	308	295.5	295	291.5	289.5	287.5	287	285.5	280	278.5	277.5	277	276.5	276	274	274	273	272	272
	Result No.	¦	7	٣	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P01805 rattus norv P01756 mus musculu										
HV01_RAT HV12_MOUSE	HV3A HUMAN	HV3K HUMAN	HV40 MOUSE	HV14 MOUSE	HV3T_HUMAN	HV51 MOUSE	HV38 MOUSE	HV3C_HUMAN	HV41 MOUSE	HV54_MOUSE
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142	122	126	119	117	116	118	119	117	117	117
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37.9	37	37	37	36	36	36	36	36	36	36
272 37.										

## ALIGNMENTS

			09
PRT; 116 AA. ed) sequence update) amnotation update) 3 precursor. a; Craniata; Vertebrata; Euteleostomi; a; Sciurognathi; Muridae; Murinae; Mus.	1=2499654; V., Lebecque S.G., Gearhart P.J.; mutation in immunoglobulin VH genes during onse."; 119(1989). SEQUENCE BELONGS TO THE VH3660 SUBFAMILY. 11ike. MHC.	Signal; 3D-structure.  IG HEAVY CHAIN V REGION 1B43. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3. BY SIMILARITY. MW; 1CB547253681FF74 CRC64;	ore 543; DB 1; Length 116;  ed. No. 7e-46;  Mismatches 7; Indels 0; Gaps  DESGPULVKPSQSLSLTCTVTGYSITSDHAWSMIRQFP  [
J MOUSE STANDARD; 532; NOV-1990 (Rel. 16, Last seq NOV-1990 (Rel. 16, Last seq SEB-2003 (Rel. 42, Last ann heavy chain V region 1843 p misculus (Mouse). aryota; Metazoa; Chordata; maila; Eutheria; Rodentia; I_TaxID=10090;	TCE FROM N.A.  =BALB/CJ,  WE=89279149; PubMec  1.S., Mallpiero U.  1.Med. 169:2007-20;  SCELLANBOUS: THIS  SCELANBOUS: THIS  SCENANBOUS: THIS  SCENABOUS: THIS  SC	Pram; Proud,; 199; 1. SMART; SMO0406; IGV; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signa; SIGNAL 1 18 16 16 DOMAIN 19 48 FF DOMAIN 49 53 CC DOMAIN 68 84 67 FF DOMAIN 68 116 FF DISULPID 40 114 B'S NON_TER 116 AA; 13158 MW;	Ouery Match Best Local Similarity 90.5%; Pr. Matches 105; Conservative 4;  1 MRVLILLMLFTAFPGILSDVQL
A H V 6 M M M M M M M M M M M M M M M M M M	R R R R R R R R R R R R R R R R R R R	S F F F F F F F F F F F F F F F F F F F	

RESULT 2

FRAMEWORK-3

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137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                               _HV60_MOUSE
P18531;
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Matches 97;
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SEQUENCE
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                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Mamno-acid Sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=17244979; PubMed=268248; Hood L., Margolies M.N., Givol D., Zakut R.; Unpublished results, cited by: Unpublished results cited by: Padlan E.A., Davies D.R., Peter I., Givol D., Wright C.; Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
-!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
                                                                                                                                                                                                                               SEQUENCE OF 1-31.
MEDLINE=7809475; PubMed=414225;
Jilka N.L., Petka S.;
Maino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain.";
                                                                                                                                                          MEDLINE-89238351; PubMed-2497341;
Rinfret A., Horne C., Dorrington K.J., Klein M.;
"Cloning, sequencing and expression of the rearranged MOPC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V REGION MOPC 315.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
                                  21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
           137 AA
                                                                       Ig heavy chain V region MOPC 315 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HASP, PO1825, 7FAB.

InterPro; IPR007110; Ig-like.

InterPro; IPR03006; Ig_W.

InterPro; IPR03596; Ig_W.

Pfam; PF00107; ig; 1.

RMART; SM00406; IGV; 1.

RP0SITE; PS50835; IG_LIKE; 1.

MIRMUNOGLOBULIN V region; Signal.

T SIGNAL

19 137 IG HE
FRAME
                                                                                                                                                                                                       401. Immunol. 26:431-434(1989)
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            STANDARD;
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54
68
84
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                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 19-136.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISION TO 53
                                                                                                                                                                                               gene segment.
            MOUSE
                     P01822;
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BALDINE=BALB/CJ;

BESTSAIN=BS279149; PubMed=2499654;

Levy N.S. Malipiero U.V., Lebecque S.G., Gearhart P.J.;

Levy N.S. Malipiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes during

"Early onset of somatic mutation in immunoglobulin VH genes during

"The primary immune response.";

J. Exp. Med. 169:2007-2019(1989).

PIR, JT0509; HVMS31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
G -> GG (IN REF. 1; CAA30727).
G -> H (IN REF. 2).
G -> H (IN REF. 4).
N -> D (IN REF. 4).
MISSING (IN REF. 4).
                                                                                                                                                                                                                                                                                             74.9%; Score 538; DB 1; Length 137; 73.7%; Pred. No. 2.6e-45; ive 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION M315.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 510; DB 1; Length 116;
Pred. No. 1.1e-42;
8; Mismatches 11; Indels
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COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                              15399 MW; FB3828304C2B81DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region M315 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596, Ig_W.
Pfam; PF00047; ig; 1.
SMART; SMO0406, IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LYYFDYWGQGTTLTVSS 137
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83.6%;
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HV43 MOUSE
P01819;
                                                                                            idiotype.";
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 SY REAL TRANSPORT OF THE SY AND T
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TEATLY onset of sometic mutation in immunoglobulin VH genes during
the primary immune response.";
J. Exp. Mad. 169:2007-2019(1989).
-!- SMILANITY: Contains 1 immunoglobulin-like domain.
PIR; JT0510; HVMS73.
R PIR; JT0510; HVMS73.
R InterPro; IPR003106; Ig_MHC.
R InterPro; IPR003596; Ig_MHC.
R InterPro; IPR003596; Ig_MHC.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 1.
R Immunoglobulin V region; Signal.
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                                                                                              61 GNKLEWMGYISYDGSNNYNPSLKNRISITRDISKNQFFLKLNSVTTEDTATYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                            GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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IG-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
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117 AA; 13223 MW; 1595517827F976BE CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                       Ig heavy chain V region 733 precursor.
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MEDLINE=89279149; PubMed=2499654;
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Best Local Similarity 74.4
Matches 87; Conservative
                                                                                                                                                                                                          STANDARD;
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>117
115
115
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                        HV62 MOUSE
P18533;
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NON TER
SEQUENCE
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HV47_MOUSE
                                                                                                                                                                                      HV62_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
                        Juszczak E.C., Margolies M.N.; "Amino acid sequence of the heavy chain variable region from the A/J mouse anti-arsonate monoclonal antibody 36-60 bearing a minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGE TARRECT THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.7%; Score 450; DB 1; Length 11 Best Local Similarity 74.8%; Pred. No. 6.8e-37; Matches 89; Conservative 12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA; 12734 MW; 38DC0E0E3F5075B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region MOPC 141 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure.
NON TER 113 113
MEDLINE=84024551; PubMed=6414509;
                                                                                                                                                              Biochemistry 22:4291-4296(1983)
                                                                                                                                                                                                                                                                                                                      PIR; A02098; G2MS60.
PDB; 1J10; 18 FEB-03.
PDB; 1J1X; 18 FEB-03.
PDB; 1J1X; 18 FEB-03.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
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InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 66 EWIGEINHSGSTNYKTSLKSRVTISLDTSKNLFSLKLSSVTAADTAVYYCARGLLRGGWN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLOLNSVTTGDTSTYYCARSLAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ILLWLFTAF.PGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88176921; PubMed=2451244; Schiner L.A.; Schwager J., Mikoryak C.A., Steiner L.A.; Mikoryak C.A., Steiner L.A.; Mikoryak C.A., Steiner L.A.; Manino acid sequence of heavy chain from Xenopus laevis IgM deduced from cDNA sequence: implications for evolution of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION XIG14. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nati. Acad. Sci. U.S.A. 85:2245-2249(1988).
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15080 MW; EBC467105C00732E CRC64;
                                                                                                                                                                                                                                                                                                                               70.357.
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 47, Last annotation update)
1g heavy chain V region XIG14 precursor (Fragment).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.1%; Score 338; DB 1; 50.7%; Pred. No. 5.7e-26; tive 20; Mismatches 44;
                                                                                                                                                                                  EMBL, J03632; AAA49791.1; -..
PIR, B31933; B31933.
HSSP; POIRB10; ZEBA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Igf; 1..
SNART; SM00406; IGV; 1..
PROSITE; PS50835; IG_LIKE; 1..
Immunoglobulin V. region; Signal.
NON TER .
                                                                                                                                                            121 ----TTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                    1 MRVLILLWLFTAFPG-ILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQF
                                                                                                                                                                                                                                                                                                                                         1 MAVLALLFCLATFPSCILSQVQLKESGPGLVAPSQSLSITCTVSGFSLTG-YGVNWVRQP
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                                                                                                                                                                                                                                                                            11; Gaps
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MEDLINE-85205332; PubMed=3922855;
Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
Kaco A., Ishihara T., Nishimura Mamuna Immunoglobulin heavy chain gene with a novel directrepeat sequence in 5' flanking region.";
Gene 33:181-189(1985).
PIR; A02101; G1HUH2.
HSSP: P01825: 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V-II REGION ARH-77. V SEGMENT. D SEGMENT. J SEGMENT. BY SIMILARITY.
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و
                                                                                                                                      IG HEAVY CHAIN V REGION MOPC 141. IG-LIKE.
                                                                                                                                                                                                                                       Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 377.5; DB 1; Length 146; llarity 56.7%; Pred. No. 9.5e-30; Conservative 16; Mismatches 36; Indels 9
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16228 MW; 8D7FD52BB218171F CRC64;
                                                                                                                                                                                                 15759 MW; 8E47A7CB3706D30A CRC64;
                                                                                                                                                                                                                                     53.6%; Score 384.5; DB 1;
56.2%; Pred. No. 2e-30;
iive 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, F01825, 7FAB.

GO, GO:0005576; C:extracellular; NAS.

GO, GO:0005823; F:antigen binding activity; NAS.

GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V-II region ARH-77 precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 YYYGRS-DKYFTLDYWGQGTSVTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00047; ig; 1. SMART; SMO0406; IGv. 1. PROSITE, PSS0835; IG LIK: 1. Immunoglobulin V region; Signal.
                                      Pfam; PF00047; ig; i. "-
SMART; SM0406; IGv; i. PROSITE, PSS0835; IG LIKE; I. 
Immunoglobulin V region; Signal.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                            82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                   144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AA;
                                                                                                                                                                                                                                                         Best Local Similarity
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Best Local Simi
Matches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 HUMAN
P06331:
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NON TER
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                       20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN 79
                                                    2 VQLEQSGPGLVRPSQTLSLTCTVSGSTFSNDY-YTWVRQPPGRGLEWIGYVFYHGTSDDT 60
                                                                                                                                                                         61 TPLRSRVTMLVDTSKNQFSLRLSSVTAADTAVYYCARNLI-AGCIDVWGQGSLVTVSS 117
                                                                                                                                         PSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81012133; PubMed-6774258; Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.; Turosawa Y., Roeder W., Roe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION PJ14.
IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region PJ14 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; V00767; CAA24148.1; -.
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                                                                                                                                                                                                                                                                                                                                     STANDARD;
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>115
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PDB; 43C9; 24-JUL-02.
PDB; 43CA; 24-JUL-02.
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1G7J; 17-JAN-01
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                                                                                                                                                                                                                                                                                                                                  _HV44_MOUSE
P01820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=78066916; PubMed=618887; Saul F.A., Amzel L.M., Poljak R.J.;
"Preliminary refinement and structural analysis of the Fab fragment from human immunoglobulin new at 2.0-A resolution.";
J. Biol. Chem. 253:585-597(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=77242302; PubMed=407927;
Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
Amino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New).";
Biochemistry 16:3412-3420(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR, A90404; GIHUNM. PDB; 7FAB; 31-JAN-94. GJHUNM. GO; GO: 0005376; C: extracellular; NAS. GO; GO: 0003823; F: antigen binding activity; NAS. GO; GO: 0009823; F: antigen binding activity; NAS. InterPro; IPR09110; Ig-like. InterPro; IPR09110; Ig-like. InterPro; IPR091066; Ig-WC. InterPro; IPR091066; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12790 MW; 2DA47B509562D237 CRC64;
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55.1%; Pred. No. 6.1e-26;
iive 25; Mismatches. 26,
                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
IIG heavy chain V-II region NEWM.
Homo sapiens (Human).
                                                                                                                                                                                                 117 AA
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124 MDYWGQGTSVTVSS 137
                                   122 FDYWGQGTMVTVTS 135
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Best Local Similarity 55.1
Matches 65; Conservative
                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                              HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSPSLKSRLTVTRDTSKNQVVLTMTNMDPVDTATYYCVHRHPRTLAFDVWGQGTKVAVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 VOLQESGPVLVKPSQSLSLTCTVTGYSITSDH-AWSWIRQFPGNKLEWMGYISY-SGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VILKENGPILVKPTETLILICTLSGLSLITDGVAVGWIRQGPGRALEWLAWLLYWDDDKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 YNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS
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MEDLINE=82075900; PubMed=6273429;
Kataoka T., Nikaidon T., Miyata T., Moriwaki K., Honjo T.;
"The nucleotide sequences of rearranged and germline immunoglobulin VH genes of a mouse myeloma MC101 and evolution of VH genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazia, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Buthazia, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                         Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.; "Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains."; Proc. Natl. Acad. Sci. U.S.A. 64:997-1003(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 323; DB 1; Length 121; 52.5%; Pred. No. 1.4e-24; ive 22; Mismatches 33; Indels
                                                                                                                                                                                                                           PIR: A02093; GIHUHE.
PIR: A02093; F: Antigen binding activity; NAS.
PIR: PIR: PIR: PIR: A02093; F: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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15-SEP-2003 (Rel. 42, Last annotation up
1g heavy chain V region MC101 precursor.
Mus musculus (Mouse).
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                                    MEDLINE=70114712; PubMed=5264153;
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PIR, A02096, G1MS10.
HSSP, P01772; 2FB4.
InterPro, IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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P01821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 NPSLRGRVTISVDTSRNQFSLNLRSMSAADTAMYYCARGNPPPYYDIGTGSDDGIDVWGQ 121
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20 VOLÕESGPVLVKPSQSLSLTCTVTGYSI-TSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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21-Jul., 1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-II region HE.
Homo saplatens (Human).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE=82222235; PubMed=6806818;
Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
Tomplete amino acid sequence of the delta heavy chain of human immunoglobulin D.";
Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02099; D2HUWA.
HSSP; PO1825; FRAB.
GO/GOSUIteDB; PO24.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:000595; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
R InterPro; IPR00710; Ig-like.
R SMART; SM00406; IG-V.
R PROSITE; PS50835; IG-LIKE; I.
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                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-II region WAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 51.6%; Pred. No. 5e-25
Matches 66; Conservative 19; Mismatches
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                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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129 AA;
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P01818;
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Query Match
Best Local Simil
Matches 64; C
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      1 MRVLILLWLFTAFPG-ILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQF 59
                                                                                                                                                                                                                                                                                                                                                                           60 PGKGLEWLGVIWSGGSTDYNAAFISRLSISKDNSKSQVFFKMNSLQSNDTAIYYCAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PGNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR 116
                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwager J., Mikoryak C.A., Steiner L.A.; "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced from cDNA sequence: implications for evolution of immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region XIGB precursor (Fragment).
Kenopus laevis (African clawed frog).
Bukaryota, Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
NCBL TaxID=8355;
                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                    IG HEAVY CHAIN V REGION MC101. IG-LIKE.
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                                                                                                                                                                                                                                                            44.0%; Score 316; DB 1; Length 11
53.8%; Pred. No. 6.5e-24;
ive 22; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domains.";
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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                                                                                                                                                                                                                      116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;
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PIR; A31933; A31933.
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InterPro; IPR00110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PPR0047; ig; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
NON TER
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; ig_1.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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Best Local Similarity 53.8%;
Matches 63; Conservative
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116
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P20956;
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SEQUENCE
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Heavy chains.;

Biochem. J. 117:641-660(1970).

L. MISCELLANGOUS: THIS CHAIN WAS OBTAINED FROM IGGI ISOLATED FROM THE SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINENIA.

-!- SIMILARITY: Contains I immunoglobulin-like domain.

PIR, A02091; GHHUDW.

RHSP: P01789; IMCP.

GO; GO:0005876; C:extracellular; NAS.

GO; GO:0008823; F:antigen binding activity; NAS.

GO; GO:0008823; F:antigen binding activity; NAS.

GO; GO:0008855; C:extracellular; NAS.

RG; GO:0008856; C:extracellular; NAS.

RG; GO:0008856; C:extracellular; NAS.

RG; GO:0008856; C:extracellular; NAS.

RG; GO:0004871; ig: 1.

PROSITE: PSS0835; IG LIKE; 1.

PROSITE: PSS0835; IG LIKE; 1.

RG-11KF.

RM-11KF.

RM-11KF.
                                                                                                                                                                                                                                                                                 62 LEWIGVVRTDGSTAIADSLKNRVTITKDNGKKQVYLQMNGMEVKDTAMYYCTSTLAGTAG 121
                                                                                                                                                                                                                                                  64 LEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTA 123
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                                                                                                                                                            4 IFVIFMFFSPSCILSQT-LQESGPGTVKPSESLRLTCTVSGFELTSYYV-WIRQPPRKT
                                                                                                                         4 LILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNK
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MEDILNE=70258837; PubMed=5449120;

Press E.M., Hogg N.M.;

"The amino acid sequences of the Fd fragments of two human gamma-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
43.5%; Score 312.5; DB 1;
llarity 47.4%; Pred. No. 1.7e-23;
Conservative 26; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V-II region DAW.
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P01816;
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homo sapien
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1 MRVLILLWLFTAFPGILSDV.....LARTTAMDYWGQGTSVTVSS 137
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## ALIGNMENTS

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61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLAR 120
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                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020191, AAH02091.1;
INTERPY: PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 Kba protein.
Mus musculus (Mouse).
                                                    479 AA
                                                      PRT,
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 2.
                                                      PRELIMINARY;
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RESULT 1
Q99M22
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В

musculu sapien sapien

homo homo Q99ng4 mus Q9ul75 homo

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Q8tc63 homo e Q8izd7 homo e Q9u196 homo e Q99131 mus n

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TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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8 K R R S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 PGKGLEWLGVIWTGGVTNYNSALKSRLSISKDNSKSQVFLKMNSLQTNDTARYYCARDSN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRVLILLWLFTAFPG-ILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidee; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Lung;
Strausberg N.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC016369; AAH161699.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007306; Ig_MHC.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB=Colon;
Strauberg R.;
Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011181; AAH11181.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003506; Ig_MHC.
InterPro; IRR003506; Ig_MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; ĪGv; 1.
PROSITE; PSG0835; IG_LIKE; 4.
PROSITE; PS00290; IG_MC; 2.
SEQUENCE 482 AA; Ī1865 MW; 312E01F9C1BC7F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 AA
                                                                                                                                                                                                                                                                                    482 AA
                             121 TTAMDY-----WGQGTSVTVSS 137
                                                                                             116 --SRGYSWFPNWGQGTLVTVSA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown (Protein for MGC:18822).
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                                                                                                                                                                                                                                                                                PRELIMINARY;
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Q96KX8
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62 NKLEWMGYISYSGITTYNPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCAR----S 117
                                                                                                                                                                                                                                                                                                                                                                                               64 KGLEWIANTYYSGITYYNPSLKSRVTISVDTSKNQLSLKVRSVTAADTAVYFCARHGYSR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KLEWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARS--LAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                  4 LWFFLLLVAAPRWVLSQLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSI-TSDHAWSWIRQFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                              9,
                                                                                                                                    Query Match 54.8%; Score 393.5; DB 4; Length 496; Best Local Similarity 60.0%; Pred. No. 5.3e-32; Matches 84; Conservative 16; Mismatches 31; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
53.8%; Score 386.5; DB 4; Length 613;
Best Local Similarity 61.3%; Pred. No. 3.6e-31;
Aatches 84; Conservative 15; Mismatches 31; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Straubberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011857; AAH11857.1; -
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003006; Ig-MrC.
InterPro; IPR003596; Ig-N.
Ffam; PR00047; ig; 5.
SWART; SP00047; ig; 5.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS0299; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 613 AA; 67273 MW; 31214203FBB421E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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09UL73
ID 09UL73;
AC 09UL73;
AC 01T3;
C1-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 SGRTGAIDYWGQGTLVTVSS 143
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123
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            20 VOLOESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN
                                                                                                                                                                                                                                                                                                                                Gaps
                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                  'Myosin-reactive autoantibodies in rheumatic carditis and normal
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"Clonal proliferation of IgM secreting B cell in the synovium
Behcet's patient with arthritis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
VH4 HEAVY CHAIN VARIABLE REGION.
                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MUX. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                       ; Score 382; DB 4; Length 119;
; Pred. No. 1.4e-31;
12; Mismatches 26; Indels
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF103795; AAC79084.1; -... HSSP; P01835; 7FAB. HINTERPRO; IPRO7110; IG-11ke. InterPro; IPRO3006; Ig-MHC. InterPro; IPRO3006; Ig-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 19 POTENTIAL.
20 >150 VH4 HEAVY CHAIN VARIABLE:
150 150 WW, 85664E04938AA7C9 CRC64;
                                                                                                                                                                                                                                                                                  119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH4 heavy chain variable region precursor (Fragment)
                                                                                                                                                     Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035041; AAD56277.1; -
HSSP; PO1825; 7FAB.
InterPro: IPR007110; Ig-like.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGV: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 AA
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                       53.2%;
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.4%,
"Then 79; Conservative 1
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SMART; SM00406; IGv; 1
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                                Homo sapiens (Human)
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01-MAR-2003
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NON_TER
SEQUENCE
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SEQUENCE
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64 KGLEWIGSLHNSGSDYYNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYXCAR--LGM 121
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                                                                                                                        4 LWFFLLLVAAPRWVLSQLQLQESGPGLVKPSETLSLSCTVSGGSISSTNYYWGWIRQPPE
                                                                                               7 LWLF - - - TAFP - GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITS - DHAWSWIRQFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
                                               7;
Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 52.1%; Score 374; DB 4; Length 597; Local Similarity 56.3%; Pred. No. 6.7e-30; Local Substractive 18; Mismatches 32; Indels 1
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC006180; AAH01872.1; -. EMBL; BC001872; AAH01872.1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003306; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_LIKE; 5.
Hypochetical protein:
ERQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
  52.2%; Score 374.5; DB 4; 58.8%; Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA
                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 PGTDGRYGMDVWGQGTTVTVSS 144
                                                                                                                                                                                                                                                                                             122 TAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                       122 GAFDFWGHGTMVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20,
20,
23,
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SEQUENCE FROM N.A.
TISSUE=Muscle, and Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 201-MAR-2002 (TrEMBLrel. 201-MAR-2003 (TrEMBLrel. 201-MAR-2003 (TrEMBLrel. 201-Mypothetical protein. Homo sapiens (Human).
                         Best Local Similarity 58.8
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
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63 KLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTT 122
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STRAIN=BALB/C;
MEDLINE=99169018; PubMed=9510199;
Hawlisch H., Frank R., Hennecke M., Baer
Bautsch W., Kola A., Klos A., Koehl J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 PGTDGRYGMDVWGQGTTVTVSS 144
                                                                                            -----AMDYWGQGTSVTVSS 137
                                                                                                                                   123 PGTDGRYGMDVWGQGTTVTVSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART, SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single chain Fv (Fragment) Mus musculus (Mouse).
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Les 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lymph;
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                                                                                                                                                                                                                                                   096AA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, EC002963; AAH02963.1; -- HSSP; P01825; 7FAB.
                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019235; AAH19235.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sepiene (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
51.3%; Score 368; DB 4;
Best Local Similarity 55.6%; Pred. No. 2.7e-29;
Matches 79; Conservative 18; Mismatches 33;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                   Pfam; PF00047; 1g; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG MHC; 3.
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PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
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                                                                                          SEQUENCE FROM N.A.
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                                                                                                               TISSUE=Lymph;
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Q9BU10;
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Matches
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63 GLEWIGEINHSGSTNYNPSLKSRVTISVDTSKKQLSLKLSSVNAADTAVYYCARVITRAS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LWLF---TAFP-GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Ntbl_TaxID=10090,
                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Home sapiens (Human).
Home sapiens (Human).
Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017356, AM17356.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig-MC.
InterPro; IPR005596; Ig-V.
Ffam; PF00047; ig: S.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALISRLSISKDNSKSQVFLKLNSLQTEDTATYYCARHYYKYANYAMDYWGQGTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TYNPSLKSRISITRDTSKNOFFLOLMSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVS 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLKESGPGLVAPSQSLSITCTVSGFPLTS-HGVSWVRQPPGKGLEWLGVIWGDGNTKYH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDH-AWSWIRQFPGNKLEWMG--YISYSGIT 76
                                                                                                                                                                                                                                                                                                                                                                                                                      20 VOLOESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWWIRQSPSRGLEWLGRIYYRSKWYN
  "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                               ; Score 367.5; DB 11; Length 121; ; Pred. No. 4.5e-30; 17; Mismatches 25; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.1%; Score 359.5; DB 4; Length : 61.2%; Pred. No. 3e-29; ive 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                              121 121
121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AA; 13719 MW; 56CB0612586A6529 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035039; AAD56275.1; -.
HSSP; PO1825; 774B.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; Gov. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AA
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                J. Immunol. 160:2947-2958 (1998).

ENBL; AJ22599; CAA10890.1; -
HSSP; PO1825; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03596; Ig_V.
Fram; PF00047; ig; 1.
SMART; SM00406; IGV.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                 51.2%;
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Homo sapiens (Human)
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les 75; Conserv
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SEQUENCE
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62 NKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLART 121
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                                                                                                                                                            QBTG63;
QBTG63;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.9%; Score 336.5; DB 4; Length 473;
51.1%; Pred. No. 3.6e-26;
tive 25; Mismatches 36; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Straubberg N.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC025985, AAH25985.1; -.
InterPro; IPR00923; BlueCu 1.
InterPro; IPR003506; Ig-NC.
InterPro; IPR003506; Ig-V.
Pfam; PF00047; ig; 4.
SWART; SM00406; IGV: 1.
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SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TAMDYWGQGTSVTVS 136
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nes 69; Conservative
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                                                                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
TISSUE=Kidney;
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122
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79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCA-RSLARTTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VQLQESGPVLVKPSQSLSLTCTVTGYSI-TSDHAWSWIRQFPGNKLEWMGYISYSGIT-- 76
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                               11;
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                            Query Match
45.8%; Score 328.5; DB 4; Length 130;
Best Local Similarity 55.0%; Pred. No. 5e-26;
Matches 71; Conservative 16; Mismatches 31; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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43.6%; Score 313; DB 4; Length 12
Best Local Similarity 54.2%; Pred. No. 1.8e-24;
Matches 65; Conservative 17; Mismatches 36; Indels
130 AA; 13901 MW; 036131FC6EC1551E CRC64;
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121 AA; 13695 MW; D582D450596BDD35 CRC64;
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EMBL; AF035018; AAD56254.1; -.
HSSP; P01825; PAB.
INCEPED: IPR07110; IG-11ke.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                         121 AA.
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01-MAY-2000 (TYEWBLrel. 13, Last seq
01-MAR-2003 (TYEWBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                         PRT;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Sequence 114, App Sequence 110, App Sequence 110, App Sequence 2, Appli Sequence 2, Appli

Appl App App Appl Appl App App App App

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

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Run on:

Sequence:

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APPLICANT: SATO, KOh
APPLICANT: SATO, KOh
APPLICANT: BANDIG, Mary
APPLICANT: BANDIG, Mary
APPLICANT: BANDIG, Mary
APPLICANT: BANDIG, Mary
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: BATENIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSI FICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25-ABR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25-ABR-1991
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECHOMUNICATION INFORMATION:
TELECHOME: (202) 672-5300
           US-08-672-345C-10
US-08-672-345C-11
US-08-672-345C-101
US-09-214-095D-11
US-09-214-095D-11
US-09-214-095D-102
US-09-214-095D-102
US-09-214-095D-103
US-08-672-345C-102
US-08-672-345C-102
US-08-672-345C-102
US-08-672-345C-102
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US-08-672-345C-103
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US-09-109-207C-2
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 31, Application US/08137117D
; Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECORDS: (2027.0.1.
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
JS-08-137-117D-31
                              October 22, 2003; 22:14:35; Search time 14.5303 Seconds (without alignments) 398.931 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/2/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-137-117D-69
US-08-16-717-69
US-08-466-151-5
US-08-466-151-5
US-08-466-151-5
US-08-137-117D-64
US-08-137-117D-64
US-08-137-117D-64
US-08-117-117D-64
US-08-211-080-23
US-08-211-980-23
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US-08-477-531B-5
US-08-082-842A-5
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US-09-065-059-11
US-08-672-345C-13
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-214-095D-13
US-08-308-494A-13
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US-08-466-151-7
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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Match Length
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Minimum DB E Maximum DB E

Database

Result Š. Searched:

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61 GNKLEWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVITGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                                                                                                                 61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYCARSLAR 120
                                                                                                                                                                                                                                      1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSTTSDHAWSWIRQFP
                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP
                                                                                                                                                      .
0
                                                                                                  Length 137;
                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Application US/08137117D
Sequence 69, Application US/08137117D
Sequence 69, Application US/08137117D
Sequence 69, Application US/08137117D
SEQUENCE 60, MASAY
APPLICANT: SATO, Koh
APPLICANT: SALONES, MASAY
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC.1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5-FEB-1992
FILING DATE: 25-FEB-1992
ATTOMATION NUMBER: US 5-FEB-1992
FILING DATE: 25-APR-1991
ATTOMATORY AGENT INFORMATION:
                                                                                                Query Match
100.0%; Score 718; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 137; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEGNER, Harold C. SEGISTATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TTAMDYWGOGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            , MOLECULE TYPE: protein US-08-436-717-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-137-117D-69
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                                                                                                                                                                                                                                                                                                                                    61 GNKLEWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120
                                                                                                                                                                                                                                    1 MRVLILLMLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
                                                                                                                                                                                                       1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
                                                                                                                                                         Gaps
                                                                                                                                                         .
0
                                                                                                  Query Match 100.0%; Score 718; DB 1; Length 137; Best Local Similarity 100.0%; Pred. No. 1.2e-65; Matches 137; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/08436717
Fatent No. 5817790
GENERAL INFORMATION
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Wary
APPLICANT: BALDAWA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: 0.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NEW RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53,466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                          121 TTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TTAMDYWGQGTSVTVSS 137
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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amino acid
                            , MOLECULE TYPE: protein US-08-137-117D-31
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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66 EWIGYISYSGITTYNPSLKSRVIMIRDISKNQFSLRLSSVTAADTAVYYCARSLARITAM 125
                                                                                                                                                                                                                                        65 EWMGYISYSGITTYNPSLKSRISITRDISKNOFFLOLNSVTTGDISTYYCARSLARTTAM 124
                                                                                                                                                                  5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64
                                                                                             Gaps
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
                                         Length 138;
                                                                                           17; Indels
                                            74.9%; Score 538; DB 2; 75.9%; Pred. No. 2.2e-47;
                                            Query Match 74.9%; Score 538; DB 3
Best Local Similarity 75.9%; Pred. No. 2.2e-4
Matches 101; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
PRIOR APPLICATION NUMBER: 08/541,373
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN 1995
ATTORNEY/AGENT INFORMATION:
NAWE: CATLEY, CHARLES G.
REGISTRATION NUMBER: 35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEN Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08767128; Patent No. G111079
GENERAL INFORMATION:
APPLICANT: WYLLE, DWANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 126 DYWGQGSLVTVSS 138
                                                                                                                                                                                                                                                                                                                                 125 DYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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US-08-436-717-69
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                                                                                                                                                                                                                                        65 EWMGYISYSGITTYNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAM 124
                                                                                                                                                                                                                                                                   66 EWIGYISYSGITTYNPSLKSRVTMLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAM 125
                                                                                                                                                                     6 ILEFLVATATGVHSQVQLQESGPGLVRPSQTLSLTCTVSGYSITSDHAWSWVRQPPGRGL 65
                                                                                                                                          5 ILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKL 64
                                         Length 138;
                                       74.9%; Score 538; DB 1; Length 13
75.9%; Pred. No. 2.2e-47;
tive 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING JATES.

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATOID C.
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 69, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                 125 DYWGOGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                           126 DYWGQGSLVTVSS 138
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                                            Query Match
Best Local Similarity 75.9%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
US-08-137-117D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-436-717-69
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US-08-137-117D-64
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                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                61 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYYCARCGNYPWYFDYWGQGTTLTVSS 119
                                                                                                                                                                                                                                                                    1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSY
                                                                                                                                                                                                                                           19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                       Gaps
                                                                                                                                                            74.4%; Score 534; DB 3; Length 119;
85.7%; Pred. No. 4.7e-47;
Live 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible SOFRATING SYSTEM: PC-DOS/MS-DOS SOFRAARE: WinPatin (Genetech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/466,151
FLING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
FILING DATE: 15-MAR-1995
PRIOR APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
FILING DATE: 07-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-ANG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1489
TELEFAX: 650/925-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 130 amino acids
Amino Acid
              MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                Best Local Similarity 85.7%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DNA Way
TOPOLOGY: linear
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                                                                                                                    US-08-767-128-18
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CITY: So
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79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NPSLKSRISITRDISKNQFFLQLNSVTTEDTATYYCAWVVA--YAMDYWGQGTSVTVSS 117
                                                                                                                                                                                                                                       61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAWVVA--YAMDYWGQGTSVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                          1 DVQLQESGPGLVKPSQSLSLTCTVTGYTITSDNAWNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVQLQESGFGLVKPSQSLSLTCTVTGYTITSDNAWNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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Pred. No. 5.3e-47;
8; Mismatches 6; Indels
Score 534; DB 3; Length 130;
Pred. No. 5.3e-47;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Oracleu, Paula M.
APPLICANT: Preste, Leonard G.
ITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: PO718P2C1D:
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1991-08-14
SEQ ID NO S: 64
SEQ ID NO S: 64
                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BRNDIG, Mary
APPLICANT: BRNDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANT
TITLE OF INVENTION: INTERLEUKIN-6 RECE
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/08466163B
; Patent No. 6329509
  74.48;
86.68;
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86.6%;
                         Best Local Similarity 86.69
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.6
Matches 103; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007-5109
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61 ITTYNPSLKSRVTWLRDTSKNQFSLRLSSVTAADTAVYYCARSLARTTAMDYWGQGSLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123
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APPLICANT: SHINAWURA, TOSHIRO
APPLICANT: TAKI, SHINSUKE
APPLICANT: TAKI, SHINSUKE
APPLICANT: TAKI, SHINSUKE
APPLICANT: TITLE OF INVENTION: POLYBEPTIDES CAPABLE OF BINDING TO HEI
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, WAIER & NEUSTADT,
ADDRESSEE: OBLON, SPIVAK, WCLELLAND, WAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.4%; Score 527; DB 2; Length 12 Best Local Similarity 79.7%; Pred. No. 2.5e-46; Matches 98; Conservative 13; Mismatches 12; Indels
      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                               USCUTWARE: Patentin Release #1.0, Version SCOTWARE: Patentin Release #1.0, Version APPLICATION DATA: APPLICATION NUMBER: US/08/436,717 FLING DATE: CLASSIFICATION 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/137,117 FILING DATE: 20-DEC-1993 APPLICATION NUMBER: WO PCT/JP92/00544 FILING DATE: 24-APR-1992 PRIOR APPLICATION NUMBER: JP 4-32084 FILING DATE: 19-FEB-1992 PRIOR APPLICATION NUMBER: JP 3-95476 FILING DATE: 25-APR-1991 ATPRNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/07956399
Patent No. 5876717
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 123 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-436-717-64
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 S.
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 VSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.4%; Score 527; DB 1; Length 123; 79.7%; Pred. No. 2.5e-46; Live 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHITA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
1TILE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/137,117D FILING DATE: 0.DEC-1993 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUMPER
                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 123 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-64
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 VSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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79 NPSLKSRISITRDISKNOFFLOLNSVITGDISTYYCARSLARTTAMDYWGQGTSVTVSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                               19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                                                                                                                                                                                                                                                                                                          ..
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.7%; Score 500.5; DB 1; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/08211980
Patent No. 566559
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
APDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606

MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                         TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 114 amino acids
amino acid
                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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US-08-211-980-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 YNPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 SDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 518.5; DB 2; Length;
Pred. No. 4.4e-45;
8; Mismatches 12; Indels
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/111,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-111-080-23
Sequence 23, Application 08/111080
Sequence 23, Application 08/111080
Patent No FSS8065
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
WUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                           CURREA,

PEDIGORIE 1992,
FILING DATE: 1992,
FILING DATE: 1992,
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ODLON, NO. 586717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-220
TELERAX: (703) 413-220
TELERAX: (703) 413-220
TELERAX: 248855 OPAT UR
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TVPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,562
FILING DATE: 22-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
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Best Local Similarity 82.5%;
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NPSLKSRISITRDTSKNLFFLQLSSVTSEDTATYYCARG-----SFGDWGQGTLVTVSA 114
                                                                                                                                                          79 NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLOESGPGLVKPSOSLSLTCTVTGYSITSDYAWNWIROFPGNKLEWMGYISYSGSTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                                                                   19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.7%; Score 500.5; DB 5; Length 114; 81.5%; Pred. No. 1.1e-43; ... 1.1ve 8; Mismatches 9; Indels 5.
81.5%; Pred. No. 1.1e-43;
tive 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                              Sequence 23f Application PC/TUS9307967
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICEATION DATA:
APPLICATION NUMBER: PCT/US92/07111
APPLICATION NUMBER: PCT/US92/07111
PILOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR-193
ATTORNEY/AGENT INPORMATION:
NAME: BOTUN, Michael F.
REGISTATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 31629
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 000000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 69.7
Best Local Similarity 81.5
Matches 97; Conservative
                       97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein PCT-US93-07967-23
  Best Local Similarity
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CLASSIFICATION:
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                         Matches
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RESULT 14 US-09-170-769A-2

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APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: MORIATRY, Ann
APPLICANT: MORIATRY, Ann
APPLICANT: TOBIAS, Peter
TILLE NETERIORS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
FILE REPERENCE: SCRIPL140: 08/09/170,769A
CURRENT APPLICATION NUMBER: US/09/170,769A
CURRENT FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/070,160
PROFINARE: PALENT OBJECT: 1993-05-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENT VERSION 3:0
SEQ ID NO 2
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LELQQSGPGLVKPSQSLSLTCTVTGYSITSDSAWNWIRQFPGNRLEWMGYISYSGSTSYN 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 VQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ;
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Pred. No. 3.6e-43;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: WAKATA, Hideo
APPLICANT: OKUWNEA, Ko-
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09065059; Patent No. 6068841; GENERAL INFORMATION:
Sequence 2, Application US/09170769A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-42,368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.5%;
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph. D., Daniel
REGISTRATION UMBER: P-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGANISM: Murine US-09-170-769A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Search completed: October 22, 2003, 22:20:50 Job time: 15:5303 secs

Sequence 1, Sequence 70,

Sequence 70, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appl Sequence 11, Appl Sequence 102, Appl Sequence 119, Appl Sequence 119, Appl Sequence 110, Appl Sequence 12, Appl Sequence 11, Appl Sequence 12, Appl

Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

Sequence 6, A Sequence 145, A Sequence 5, A Sequence 5, A Sequence 7, A

Minimum DB Maximum DB

Seguence:

Run on:

Database :

Result No.

114321098765432

Sequence 8,

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NPSLKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLARTTAMDYWGQGTSVTVSS 137
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Patent No. US20010033842A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US

CURRENT APPLICATION NUMBER: US/09/802,077

CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 534; DB 9; Length 130;
Pred. No. 3.8e-43;
8; Mismatches 6; Indels
5 US-10-184-300A-1

0 US-09-144-886-70

US-09-802-096-7

US-09-802-096-7

1 US-09-940-7278-10

1 US-09-940-7278-10

1 US-09-940-7278-10

1 US-09-940-7278-10

1 US-09-940-7278-11

1 US-09-940-7278-11

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1 US-09-940-7278-11

US-09-92-171-2

US-09-92-077-3

US-09-92-077-3

US-09-92-171-2

US-09-92-171-2

US-09-92-171-2

US-09-92-179-3

US-09-97-171-680-5

US-09-874-141-7

US-09-874-141-7

US-09-874-141-7

US-09-874-141-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR PELICATION NUMBER: US 08/405,617
PRIOR PELICATION NUMBER: US 08/185,899
PRIOR PELING DATE: 1995-03.15
PRIOR PELING DATE: 1994-01-26
PRIOR PELING DATE: 1992-08-14
PRIOR PELING DATE: 1992-08-14
PRIOR PELING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PELING DATE: 1992-05-07
PRIOR PELING DATE: 1992-05-07
PRIOR PELING DATE: 1991-08-14
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86.6%;
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Best Local Similarity 86.6'
Matches 103; Conservative
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US-09-802-077-5
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458.5
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Sequence 36, Appl
Sequence 59, Appl
Sequence 53, Appl
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Sequence 258, App
Sequence 13, Appl
Sequence 2, Appli
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Sequence 270, App
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Sequence 5, Appli
Sequence 5, Appli
Sequence 58, Appli
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902.237 Million cell updates/sec
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                                                                                                                                                                                                                    US-09-114-285A-31
718
1 MRVLILLWLFTAFPGILSDV.......LARTTAMDYWGQGTSVTVSS 137
                                                                                                                                     October 22, 2003, 22:16:46 ; Search time 25.428 Seconds
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(ggn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

(ggn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

(ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

(ggn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-925-179-5
US-09-144-886-58
US-09-144-886-59
US-09-874-141-53
US-10-184-300A-3
US-10-207-655-260
US-10-207-655-270
US-09-858-349-2
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US-09-940-727B-13
US-10-184-300A-2
US-09-874-141-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-802-077-5
US-09-802-096-5
                                                                                                                                                                                                                                                                                                                                                             629382 segs, 167460630 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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length: 2000000000
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2; Gaps

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Sequence 36, Application US/10310674A
Publication No. US20030166860A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Femily
FILE REFERENCE: 00140/004001
CURRENT APPLICATION NUMBER: US/10/310,674A
CURRENT APLICATION DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 36
LENGTH: 121
LENGTH: 121
                                                                                                                                                                                                                                                                         61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAWVVA--YAMDYWGQGTSVTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/09144886

Patent No. US2002015514A1

GENERAL INFORMATION:
APPLICANT: Marks, James D.

APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Betulinum Neurotoxins
FILE REFERENCE: 2500.1170NS
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58

LENGTH: 115
                                                                                                                                                                1 DVQLQESGPGLVKPSQSLSLTCTVTGYTITSDNAMNWIRQFPGNKLEWMGYINHSGTTSY
                                                                                                                                  19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone; OTHER INFORMATION: 1E8 region VH epitope 1
US-09-144-886-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.6%; Score 521; DB 10; Length 115; Best Local Similarity 86.6%; Pred. No. 5.7e-42; Matches 103; Conservative 3; Mismatches 9; Indels 4
                      Length 130;
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                                                                          Indels
                      Score 534; DB 11;
Pred. No. 3.8e-43;
8; Mismatches 6;
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US-10-310-674A-36
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Pred. No. 6e-42;
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                           74.4%;
86.6%;
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ORGANISM: Artificial Sequence
FEATURE:
                                                    Best Local Similarity 86.0
Matches 103; Conservative
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Best Local Similarity
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                              Query Match
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                                                                                                              Sequence 5, Application US/09802096

Batent No. US20010038839A1

GENERAL INFORMATION:
APPLICANT: Jazdieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TILE OF INVENTION NUMBER: US/09/802,096
CURRENT FILING DATE: 201-03-08
FRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1995-03-15
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-05-07
PRIOR PAPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
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; Publication No. US20030044858A1
; GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Anti-1gE Antibodies (as amended)
FILE REFERENCE: POTABP2CIDICUS
CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT APPLICATION NUMBER: US 08/466,163
; PRIOR PILING DATE: 1995-06-06
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1995-03-15
; PRIOR FILING DATE: 1995-03-15
; PRIOR FILING DATE: 1995-08-14
; PRIOR FILING DATE: 1992-08-14
; PRIOR FILING DATE: 1992-08-14
; PRIOR FILING DATE: 1992-08-14
; PRIOR FILING DATE: 1991-08-14
; SEQ ID NO 5
; LENGTH: 130
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Pred. No. 3.8e-43;
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                                                                                                      US-09-802-096-5
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; ORGANISM: Homo sapiens
US-09-874-141-53
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APPLICANT: PAN, LI-ZHEN
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: RASTETTER, WILLIAM H.
APPLICANT: KLOETZER, WILLIAM S.
TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0280632
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR PRIOR DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 53
LENGTH: 140
TYPE: PRT
                                                                                                                            79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTT--AMDYWGQGTSVTVS 136
                                                                                                                                                          61 NPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARDWPRPSYWYFDVWGAGTTVTVS 120
                                                                    1 DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYIRYSGSTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAMSWIRQFPGNKLEWMGYISYSGITTY 78
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                                           19 DVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFPGNKLEWMGYISYSGITTY
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      2; Gaps
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Patent No. US/0020155114A1

GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.1170SO
CURRENT APPLICATION UNMER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone; OTHER INFORMATION: 1G7 region VH epitope 1
US-09-144-886-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.1%; Score 518; DB 10; Length 115; 86.6%; Pred. No. 1.1e-41; ive 2; Mismatches 10; Indels
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  12; Indels
  6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 59
LENGTH: 115
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Best Local Similarity 86.6
Matches 103; Conservative
  101; Conservative
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Matches
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                                                                                                                          1 MRVLILLWLFTAFPGILSDVQLQESGPVLVKPSQSLSLTCTVTGYSITSDHAWSWIRQFP 60
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                                                                                                                                                              1 MWULSLLYLLTALPGFLSEVQLQESGPSLVKPSQTLSLTCSVTGDSITNGF-WIWIRKFP
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                                                                Gaps
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APPLICANT: Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
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   DB 11; Length 140;
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                                                             Indels
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LOCATION: ()..()
OTHER INFORMATION: Synthetic construct of 3B6DIVHv7
71.4%; Score 512.5; DB 11; 75.5%; Pred. No. 4.5e-41; Live 12; Mismatches 19;
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Fublication No. US20030124056A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
CURRENT APPLICATION NUMBER: US/10/184,300A
CURRENT FILING DATE: 2002-10-29
PRIOR PILING DATE: 2002-10-26
PRIOR PAPLICATION NUMBER: US 60/301,154
PRIOR FILING DATE: 2001-0-6
PRIOR FILING DATE: 2001-0-6
PRIOR FILING DATE: 2001-0-6
PRIOR FILING DATE: 2001-0-6
PRIOR PRILING DATE: 2001-0-6
PRIOR PRILING DATE: 2001-0-6-27
NUMBER OF SEQ ID NOS: 12
SOUTHAND APPLICATION NUMBER: US 60/300,947
NUMBER OF SEQ ID NOS: 12
SOUTHAND APPLICATION NUMBER: US 60/300,947
NUMBER OF SEQ ID NOS: 12
SOUTHAND APPLICATION NUMBER: US 60/300,947
NUMBER OF SEQ ID NOS: 12
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; Publication No. US20030118592A1
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 75.5$
Matches 105; Conservative
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Matches 94; Conserv
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61 NPSLKNRISITRDTSKNQFFLKLNSVTTEDTATYYCARXXXXXXXXDYWGQGTTVTVAA 120
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; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Ledbetter, Jeffrey A.
; TTLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; TTLE TERERENCE: 39069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SEQ ID NO 258
; SEQ ID NO 258
; LENGTH: 119
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REPERENCE: 0575/51400-B
CURRENT PILLOATION NUMBER: US/09/940,727B
CURRENT PILLING DATE: 2002-09-04
PRIOR PELLOATION NUMBER: 09/214,095
PRIOR FILLING DATE: 1998-12-28
PRIOR FILLING DATE: 1998-06-25
PRIOR FILLING DATE: 1997-06-25
PRIOR FILLING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
                                                                                                                                                      Query Match 69.3%; Score 497.5; DB 9; Best Local Similarity 78.3%; Pred. No. 1.2e-39; Matches 94; Conservative 9; Mismatches 16;
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SEQ ID NO 13
LENGTH: 117
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (99)...(107)
; OTHER INFORMATION: variable
US-09-858-349-2
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US-09-940-727B-13
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Patent No. US20020012909A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SMALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT APPLICATION DAYS: 16

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3:1
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 30069-401C.
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SSOFTWARE: Patentin version 3.0
LENGTH: 550
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69.4%; Score 498; DB 15;
Best Local Similarity 79.2%; Pred. No. 2.2e-39;
Matches 95; Conservative 10; Mismatches 15;
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; OTHER INFORMATION: fusion polypeptide
US-10-207-655-260
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                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 95; Conservative
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version
SEQ ID NO 260
LENGTH: 266
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LENGTH: 136
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US-09-858-349-2
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                                                                                                                                                                                                                                       79 NPSLKSRISITRDTSKNOFFLQLNSVTTGDTSTYYCARSLARTTAMDY-----WGQGTSV 133
                                                                                                                                                                                               1 DVQLQESGPELVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNRLEWMGYIRYSGITRY 60
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                                                                                Length 117;
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OTHER INFORMATION: Synthetic construct of 3B6DIVHv6
                                                                          Score 493; DB 11;
Pred. No. 2.6e-39;
8; Mismatches 6;
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APPLICANT: Carr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Carr, Francis J.
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
CURRENT APPLICATION NUMBER: US/10/184,300A
CURRENT FILING DATE: 2002-10-29
FRIOR APPLICATION NUMBER: DCT/AU02/00827
FRIOR FILING DATE: 2002-10-26
FRIOR APPLICATION NUMBER: US 60/301,154
FRIOR APPLICATION NUMBER: US 60/301,154
FRIOR FILING DATE: 2001-06-26
FRIOR APPLICATION NUMBER: US 60/301,154
FRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10184300A Publication No. US20030124056A1
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RASTETTER, WILLIAM H.
KLOETZER, WILLIAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
                                                                          Query Match
Best Local Similarity 78.5%;
Matches 95; Conservative
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Matches 91; Conserv
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-13
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US-09-874-141-49
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APPLICANT:
APPLICANT:
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60 GNKLEYMGYISYSGSTYYNPSLKSRISISRDTSKNQFSLKLSSVTAADTGVYXCACRSYG 119
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     COMPOSITIONS
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US-09-874-141-49
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TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, C
TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-02806.52
CURRENT APPLICATION NUMBER: US/09/874,141
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 53
SOFTWARR: PARCENTIN VET: 2.1
SEQ ID NO 49
LENGTH: 140
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Best Local Similarity 71.2%; Pred. No. 1.2e-37;
Matches 99; Conservative 14; Mismatches 23
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                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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1129.179 Million cell updates/sec
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1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA 411
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                              Copyright
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Applı , App , Appli 57, App Appli Sequence 35, Appl Sequence 259, App Sequence 269, App Sequence 257, 1 Sequence 1, Appl Sequence 8, Appl Sequence 101, 1 Sequence 2, Seguence 9 Sequence 7 Sequence 5 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 1 Description US-10-184-300A-8 US-09-940-727B-101 US-01-184-300A-7 US-01-171-681-28 US-10-171-680-28 US-09-940-727B-105 US-09-940-727B-105 US-09-940-727B-105 US-10-310-674A-35 US-10-207-655-259 US-10-207-655-269 US-10-184-300A-9 US-10-207-655-257 US-09-858-349-1 Length DB Query Match 1 269 268 2550.8 2550.8 2550.2 2557.2 2555.8 2555.8 245.6 45.6 45.6 278.6 271.4 271.4 Result o N

Sequence 48, Appl Sequence 26, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 26, Appl Sequence 27, Appl Sequence 21, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 1, Appl Sequence 27, Appli Sequence 15, Appli	
US-09-874-141 US-00-874-141 US-10-171-681 US-10-171-681 US-10-171-762 US-10-181-762 US-10-181-762 US-10-181-762 US-10-181-762 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-425-529 US-10-426-782 US-10-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-7632 US-09-96-864-761-76330-5030-50330-5	12 US-10-330-530-15 US-09-925-299-198 11 US-09-925-299-198 9 US-09-905-243-7 9 US-09-864-761-31244
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## ALIGNMENTS

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TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin
TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States
TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States
TITLE OF INVENTION DATE: DM-6956
CURRENT APPLICATION NUMBER: US/09/237,061
PRIOR APPLICATION NUMBER: 60/072,733
PRIOR PILING DATE: 1998-01-27
RINBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0 09 14 Argadastronaricaricaractronarical arganization 73 61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC caderreaddaderenddeeeredraaacerrereadrerererererereeeree 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG Gaps OTHER INFORMATION: Description of Artificial Sequence: Heavy Chain of OTHER INFORMATION: rJK094 3; Length 1420; Indels 68.4%; Score 281.2; DB 9; ilarity 81.6%; Pred. No. 8e-84; Conservative 0; Mismatches 73; Sequence 2, Application US/09237061 Patent No. US20020081624A1 GENERAL INFORMATION: ORGANISM: Artificial Sequence Query Match Best Local Similarity Matches 338; Conserv SEQ ID NO 2 LENGTH: 1420 US-09-237-061-2 TYPE: DNA gg 8 ð g δ

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Sequence 259, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TILE OF INVENTION: BINDING DOWAIN-INMUNOCIOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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APPLICANT: Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 269
LENGTH: 1665
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Pred. No. 1.2e-80;
0; Mismatches 61; Indels 0;
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polynucleotide
US-10-207-655-269
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Best Local Similarity 83.5%;
Matches 308; Conservative 0
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ORGANISM: Artificial Sequence
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                                                                                                             TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                      254 TCTCTCAAAAATCGAATCTCCATCACTCGTGACACATCTAAGAACCAGTTTTTCCTGAAG 313
                                                                                                                                                                                                            301 TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG---CT 357
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                                                      194 GGAAACAAACTGGAATGGGTGGCTATATAAGTTATGTCGGTAACAATGACTACAACCCA
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                 GGAAACAAACTGGAGTGGGATGGGCTACATAAGTTACAGTGGTATCACTACCAACCCA
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TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of
TITLE OF INVENTION: Pemily
FILE REFERENCE: 00140/00104
CURRENT APPLICATION NUMBER: US/10/310,674A
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.2
SEQ ID NO 35
LENGTH: 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-310-674A-35
; Sequence 35, Application US/10310674A
; Publication No. US20030166860A1
; GENERAL INFORMATION:
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US-09-858-349-1
; Sequence 1, Application US/09858349
; Patent No. US20020012909A1
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Best Local Similarity 84.6%;
Matches 301; Conservative (
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Pred. No. 5.6e-80;
0; Mismatches 45; Indels
                                                          61; Indels
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COTHER INFORMATION: Synthetic construct of 3B6DIVHv7
US-10-184-300A-9
Score 271.4; DB 14;
Pred. No. 1.7e-80;
0; Mismatches 61;
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APPLICANT: Carr, Hamilton, Anita A.
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 22972201700
CURRENT APPLICATION NUMBER: US/10/184,300A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: PCT/AU02/00827
PRIOR FILING DATE: 2002-10-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10184300A; Publication No. US20030124056A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 86.6%;
Matches 309; Conservative (
Query Match
Best Local Similarity 83.5%;
Matches 308; Conservative
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US-10-184-300A-9
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61 ACCTGCACTGTCACTGGCTACTCAATCACAGTGATTATGCCTGGAACTGGATACGGCAG 120
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Publication No. US20330118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069-401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 257
LENGTH: 362
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Pred. No. 1.2e-79;
0; Mismatches 55; Indels
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Gaps

3,

51; Indels

Length 354;

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55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
                                                            Score 259.4; DB 14;
Pred. No. 9.3e-77;
0; Mismatches 51; I
    ; OTHER INFORMATION: Synthetic construct of 3B6DIVHv6 US-10-184-300A-8
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Best Local Similarity 84.9%;
Matches 303; Conservative (
                                                              63.1%;
ilarity 84.9%;
Conservative (
                                                                                    Similarity
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US-09-940-727B-101
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                                                                Query Match
Best Local Simi
Matches 303;
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LENGTH: 366
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GENERAL INFORMATION:
APPLICANT: PLAKSIN, Daniel
TITLE OF INVENTION: SNALL FUNCTIONAL UNITS OF ANTIBODY HEAVY CHAIN VARIABLE REGIONS
FILE REFERENCE: 87534-2800
CURRENT APPLICATION NUMBER: US/09/858,349
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO.1
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ORGANISM: mouse hybridoma specific for H-2D + RGPGRAFVTI peptide
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Pred. No. 3.4e-77;
6; Mismatches 54;
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| Sequence 8, Application US/10184300A
| Publication No. US20030124056A1
| GENERAL INFORMATION:
| APPLICANT: Carr, Francis J.
| APPLICANT: Hamilton, Anita A.
| TITLE OF INVENTION: Carrier molecules
| FILE REFRENCE: 229752001700
| CURRENT APPLICATION NUMBER: US/10/184,300A
| CURRENT FILING DATE: 2002-10-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-26
| PRIOR FILING DATE: 2001-06-27
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: PatentIN version 3.0
| SEQ ID NO 8
                                                                                                                                                                                                                                                                         ; NAME/KEY: misc feature
; LOCATION: (295).. (320)
; OTHER HON: A or g or c or t/u
US-09-858-349-1
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Best Local Similarity 82.3%;
Matches 293; Conservative
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셤 ò g ò 8 ò TYPE: DNA ORGANISM: Artificial sequence

FEATURE:
NAME/KEY: misc\_feature
LOCATION: ()..()

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174
                                                                                                                      61 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAACTGGATACGGCAG 120
                                                                                                                                                                                                                                             121 CCACCAGGAAAGGGACTGGATGGGTTGCTACATAACCTACAGTGGTACCACTAGCTAC 180
                                                                                                                                                                                                                                                                                                          294
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                                                                                                                                                                                                                                                                                                                                                                                                                                   295 CTACAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTA 354
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TTTC----CTTACTACTACTACTGGGGCCAAGGCACCACCACACAGGTCTCTTCA 354
1 GATGTGCAGCTTAAGGAGTCGGGACCTGGCCTGGTTAAACCTACTCAGACTCTGACCTC
                                                            115 ACCTGCACTGTCACTGGCTACTCCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG
                                                                                                                                                                                   175 TITCCAGGAAACAAACTGGAGGGATGGGCTACATAAGTTACAGTGGTATCACTAC
                                                                                                                                                                                                                                                                                                          AACCCATCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE PEFERENCE: 0555/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1996-06-25
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN VEXESION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 258.2; DB 11;
Pred. No. 2.4e-76;
0; Mismatches 48;
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Publication No. US20030012781A1
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                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (7)..(426)
US-09-874-141-52
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US-10-171-681-28
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ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAACTGGATACGGCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CCACCAGGAAAGGGACTGGAGTGGATGGCCTACATAACCTACAGTGGTACCACAGCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CTGCAGTTGAATTCTCTGACTTCTGAGGACACAGCCACATATTACTGTGCAAGAGAGTGG 300
                                                                                    241 CTGCAGTTGGATTCTGTGACTGCTGAGGACACAGCCACATATTATTGTGTAAGATATCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG 174
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                                                      CTACAGTIGAATICIGIGACIACIGGGGACACGICCACAIAIIACIGIGCAAGAICCCIA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATGTGCAGCTTAAGGAGTCGGGACCTGGCTGGTTAAACCTACTCAGACTCTGACCCTC 60
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                                                                                                                           355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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                                                                                                                                                 301 TACTACGGTTCGGCT-----TACTGGGGCCAAGGGACTCTGGTCTCTGCA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.7%; Score 257.8; DB 14; Length Best Local Similarity 84.6%; Pred. No. 3.2e-76; Matches 302; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
| LOCATION: () ...()
| THER INFORMATION: Synthetic construct of 3B6DIVHv5
US-10-184-300A-7
                                                                                                                                                                                                                                                                                                  GENERAL INFOCATE, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Hamilton, Anita A.
TITLE OF INVENTION: Carrier molecules
FILE REFERENCE: 229752001700
CURRENT FILING DATE: 2002-10-29
REIOR APPLICATION NUMBER: US /AU02/00827
PRIOR FILING DATE: 2002-10-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                 Sequence 7, Application US/10184300A, Publication No. US20030124056A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                   RESULT 10
US-10-184-300A-7
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                    181
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Sequence 52, Application US/09874141

RESULT 11 US-09-874-141-52

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GENERAL INFORMATION

APPLICANT: ANDERSON, DARRELL

APPLICANT: ANDERSON, DARRELL

APPLICANT: HANNA, NABIL

APPLICANT: RASTETTER, WILLIAM H.

APPLICANT: RASTETTER, WILLIAM H.

APPLICANT: RASTETTER, WILLIAM GAPIS, COMPOSITIONS

TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION CONTAINING, AND THERAPEUTIC USE THEREOF

CURRENT APPLICATION NUMBER: US/09/874,141

CURRENT FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 TIGAATITCIGIGACTACTGAGGACACACAGACATATTACTGIGCCTGCCGCAGTTACGGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TCTGTCACTGGCGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAAATTCCCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/10171681
Publication No. US20030170233A1
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: PADLAN, Radia
APPLICANT: PADLAN, Reluardo A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF EQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.2%; Score 255.8; DB 11; Best Local Similarity 79.4%; Pred. No. 1.6e-75; Matches 331; Conservative 0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
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TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
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APPLICANT: NEWANN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 CAGCTICAGGAGTCAGGACCIAGCCTCGTGAAACCTICTCAGACTCTGTCCCTCAGCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 TCTGTCACTGGCGACTCCATCAC---TAATGGTTTCTGGATCTGGATCCGGAAATTCCCA
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Pred. No. 1.6e-75;
0; Mismatches 77; Indels 9;
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US/08/554,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 355-5620
INFORMATION FOR SEO ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 426 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 79.4%;
Matches 331; Conservative (
  Publication No. US20030175269A1
                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                        APPLICANT: BLACK, Amelia APPLICANT: HANNA, NAbil
                                                                                                                                                                                                                                                  CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ACTACGGC-----TATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                  COUNTRY: United States
ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,681
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77;
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62.2%; Score 255.8;
Best Local Similarity 79.4%; Pred. No. 1.66
Matches 331; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERNCE/DOCKET NUMBER: 012712-127
TELECOMMINICATION: INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-171-680-28
; Sequence 28, Application US/10171680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: TVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                           FILING DATE: 17-JUNE-2001
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                     : Virginia
RY: United States
22313-1404
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Alexandria
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US-10-171-681-28
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Search completed: October 24, 2003, 06:22:18
Job time : 977.625 secs
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TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                     CTACAGTIGAATICIGIGACTACTGGGGACACGICCACATAITACTGIGCAAGAICCCTA 354
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                                                                                                                   AGGACCCCGTACTTTGACTTCTGGGGCCAAGGCACCACTCTCACCGTCTCCTCA 420
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                                                                                 361 ACTACGGC-----TATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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Pred. No. 9.8e-75;
0; Mismatches 51; Indels
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JUNEAU LUNGUALION:
JUNEAU CANTILON:
JUNEAU CANTILON:
JUNEAU CANTILON:
JUNEAU CANTILON:
JUNEAU CANTILON:
JUNEAU CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR PILING DATE: 1999-7-06-25
PRIOR RILING DATE: 1996-06-25
PRIOR APPLICATION NUMBER: 09/672,345
PRIOR FILING DATE: 1996-06-25
PRIOR RILING DATE: 1996-06-25
PRIOR PILING DATE: 1996-06-15
SQOTWARE: PATENTIN VENESION 3.1
SQOTWARE: PATENTIN VENESION 3.1
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TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
TILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-940-727B-109
; Sequence 109, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
                                                                                                                                                                                     RESULT 14
US-09-940-727B-105
Sequence 105, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.0%;
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: mous
US-09-940-727B-105
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301
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47 GANAGGGGGNCGGAGCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGCACTGTCACT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.8%; Score 245.6; DB 11; Length Best Local Similarity 87.4%; Pred. No. 4.3e-72; Matches 292; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 ATGGACTACTGGGGTCAAGGAACCTCAGTCACCG 403
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PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 109
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: any nucleotide FEATURE:
NAME/KEY: misc_feature
LOCATION: (28)..(28)
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NAME/KEY: misc_feature

LOCATION: (56) \(^1.66)\)

OTHER INFORMATION: any nucleotide

US-09-940-7278-109
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OTHER INFORMATION: any nucleotide
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LOCATION: (49)...(49)
OTHER INFORMATION: any nucleotide
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OTHER INFORMATION: any nucleotide
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NAME/KEY: misc_feature
LOCATION: (21)..(21)
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TELEX: 904136
INFORMATION FOR SEQ 1D NO: 300
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
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TELEFAX: (202)672-5399
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/cgn2_6/ptcdata/2/ina/PcTUG_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PcTUG_COMB.seq:*
                    GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-135-399-1

US-09-170-769A-1

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Fatent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: DENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: Masayuki
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 STATE: 3000 K Street, N.W., Suite 500 STATE: D.C. COUTRY: USA STATE: D.C. COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOGTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE.
                                                                                                                                                                                                                                                                                                            Score 411; DB 1; L
Pred. No. 5.6e-132;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 411; Conservative
                                                                                                                                                                                    mat_peptide
STRANDEDNESS: single
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FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                       1..411
                                lineal
                                                                                                                                                                                                                     ; LOCATION:
US-08-137-117D-30
                                                                                       NAME/KEY:
LOCATION:
                         TOPOLOGY:
FEATURE:
                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-436-717-30
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                                                                                                                                                       FEATURE:
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61 CAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 411; DB 1; L
Best Local Similarity 100.0%; Préd. No. S.6e-132;
Matches 411; Conservative 0; Mismatches 0;
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 73-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 3(
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..411
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LOCATION:
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LOCATION:
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FEATURE:
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240 300

180 240

120

360

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APPLICANT: Dornburg, Ralph C.
TITLE OF INVENTION: Cell-Type Specific Gene Transfer Using
TITLE OF INVENTION: Retroviral Vectors Containing Antibody-Envelope Fusion
TITLE OF INVENTION: Proteins and Wild-Type Envelope Fusion Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. BOX 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 180
                                                                   181 AACCCATCTCTAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 ArgargererraAgrerrergracererreacedecerrecegerarecrereacedere 102
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                                                                                                                                                                   241 CTGCAGTTGAATTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGATGTGGT 300
                         AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC 294
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BE PC compatible

COMPUTER: BE PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/933,616

FLING DATE: 04-MAR-1994

ATTORNEY AGENT INFORMATION:

NAME: Muccino, Richard R.

REFERENCE/DOCKET NUMBER: UMD1-025

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 466-3407

TELECOMMUNICATION OF SEQ ID NO: 1:

SEQUIRCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08933616; Patent No. 5869331; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: DNA (genomic)
US-08-933-616-1

    836 base pairs
nucleic acid
    DEDNESS: unknown

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STATE: New Jersey
COUNTRY: USA
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                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St CITY: Minneapolis STATE: MN
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 357;
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                 LEAD BINDING POLYPEPTIDES AND NUCLEOTIDES CODING THEREFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.5%; Score 297.8; DB 3 ilarity 89.6%; Pred. No. 5.6e-93; Conservative 0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: US/08/76/,128
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 06-JUN-1995
ATJORNEY/AGENT INFORMATION:
NAME: CARLER, CHARLES G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                           US/08/767,128
                                                                                                                                                                                                                                  ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FastERE VESTER
COMPATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 86.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence

LOCATION: 1...357

CTHER INFORMATION:

US-08-767-128-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 357 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                   NUMBER OF SEQUENCES:
                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
GOEBEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 320; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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엄 ð a

300

219 240

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RESULT 6
US-09-135-121B-3
is General Department of Signation US/09135121B
j Patent No. 6334051
is GENERAL INFORMATION:
TITLE OF INVENTION: CELL TYPE SPECIFIC GENE TRANSFER USING RETROVIRAL VECTORS
TITLE OF INVENTION: CONTAINING ANTIBODY-ENVELOPE FUSION PROTEINS AND WILD-TYPE
FILE REFERENCE: 97,216-L
CURRENT APPLICATION NUMBER: US/09/135,121B
CURRENT FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: US 08/203,616
PRIOR PELING DATE: 1997-08-28
PRIOR PELING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: B6.2 gene encoding single chain antibody against hapten DNP
US-09-135-121B-3
                                                                                                                                                                                                                                                                                                                  TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAGAACCAGTACCTGCAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                          340 rigaaricigigacracigagacacacaccacararracigigadaar---arggregr 396
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                                                                                                                                        163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA
                                                                                                                                                                                                                                220 GGGAATAAACTIGAGTACATGGGGTACATAAGCTACAGTGGTAGCACTTACTACAATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 411
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Pred. No. 3.1e-88;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2%;
Matches 346; Conservative C
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsoft Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft WC
SEQ ID NO 3
LENGTH: 836
                                                                                                                                                                                                                                                                                                                                      280
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Sequence 1, Application US/08279307
Patent No. 6146885
GENERAL INFORMATION:
APPLICANT: Dornburg, Ralph C.
TITLE OF INVENTION: Cell-Type Specific Gene Transfer
TITLE OF INVENTION: Cell-Type Specific Gene Transfer
TITLE OF INVENTION: Pusion Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
CITY: Princeton
STATE: New Jersey
163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA 219
                                                                                                                                    TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                                                    280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACCACCAAGAACCAGTACTACCTGCAG 339
                                                                                                                                                                                                                         301 TIGAATICTGIGACTACTGGGGACACGICCACATATTACTGTGCAAGATCCCTAGCTCGG 360
                                                                                                                                                                                                                                                                      340 TTGAATTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGAT---ATGGTGGT 396
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                                                                          GGAAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACCAACCCA
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                                                                                                                                                                                                                                                                                                                  361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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Pred. No. 3.1e-
0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/979,619
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 84.2%;
Matches 346; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 836 base pairs
TYPE: nucleic acid
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58 GTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACC 117
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                                                                                                                  296 TACAGTIGAATICTGIGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG 355
                                                                                                                                                                                                                         608 TGCAGTTGAATTCTGTCACTACTGAGGACACAGCCACATATTACTGTGCAAGA---GGTG 664
rrccaggaaacaaacregagregarggerracgraagcracagregregregacraca 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 ACCCATCTCTAAAAGTCGAATCTCTATCACTCGAGACACAACAAGAACCAGTTCTTCC
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                                                                                                                                                                                                                                                            356 CICGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCÄCCGTCTCCTCA
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APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: OKUMURA, Ko
APPLICANT: INKATA, MOCOMI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 264.4; DB 3;
Pred. No. 1.8e-81;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: MCDermott, Will & Emery STREET: 99 Canal Center Plaza CITY: Alexandria STATE: Vire:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-065-059-12;
Sequence 12, Application US/09065059;
Patent No. 6068841
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84.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 84.2
Matches 298; Conservative
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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: USA
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                                280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAGAACCAGTACCTGCAG
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TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                      TIGAATICIGIGACTACIGGGGACACGICCACAIAITACIGIGCAAGAICCCTAGCICGG 360
                                                                                                                              340 TTGAATTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAGAT---ATGGTGGT 396
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHIMMANDA, TOSHIRO
APPLICANT: TAKI, SHIMSUKE
APPLICANT: HAMMORO, JUNJI
TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STRATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                       397 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 447
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                                                                                                                                                                             361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876/17man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-586-0
TELEFONE: (703) 413-3000
TELEFONE: (703) 413-2220
TELEFONE: (703) 413-2220
TELEFONE: (703) 413-2220
TELEFONE: TELEFONE: CHARACTERISTICS:
LENGTH: 720 base pairs
TVOFF: NUCLEIC ACID
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88.2%; Pred. No. 7.4e-86;
ive 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07956399
Patent No. 5876717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUFULOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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Best Local Similarity 88.2
Matches 314; Conservative
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US-07-956-399-1
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121 TTTCCAGGAAACAACTGGAGTGGATGGGCTACATAAGGCACATTTATGGCACTAGGTAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPOMMINICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPAX: 212-278-0400
                      APPLICANT: Landry Donald, w.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE DODRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: ANTI-COCAINE CATALYTIC ANTIBODY 51400-A-PCT-US
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Pred. No. 2.6e-79;
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                                                                                                                                                         STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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84.9%;
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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Matches 303; Conserv
GENERAL INFORMATION:
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US-09-214-095D-101
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US-08-672-345C-87
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                                   121 CCAGGAAACAAACTGGAATGGATGGGCTACATAAGCTACGATGGTAGCAATAACTACAAC 180
                                                                                                                         238 CCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTA 297
                                                                                                                                                                                                                                                     298 CAGTTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCT 357
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62 AGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGCA
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llarity 93.2%; Pred. No. 8.2e-80;
Conservative 0; Mismatches 20; Indels
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; LOCATION: (1)..(639)
US-09-170-769A-1
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Best Local Similarity
Matches 272; Conserv
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US-09-170-769A-1
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CAGCTTCAGGAGTCAGGACCTAGCCTCGTGAAACCTTCTCAGACTCTGTCCCTCACCTGT 126
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GENERAL INFORMATION:
APPLICANT: BLACK.
APPLICANT: BADLAN, Rabil
APPLICANT: PADLAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAATAAACTTGAGTACATGGGCTACATAAGTTACGGGGTAGCACTTACTACAATCCA
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                                                                                                                                                                                                                                                                                                 Length 426;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                              Score 255.8; DB 3
Pred. No. 1.9e-78;
0; Mismatches 77
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INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 426 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                 Query Match 62.2%;
Best Local Similarity 79.4%;
Matches 331; Conservative
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COUNTRY: United States
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CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                            , NAME/KEY:
, LOCATION:
US-08-554-840-28
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PADLAN, Eduardo A.
PEPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 GCTCGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                   Length 366;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                              Score 258.2; DB 3;
Pred. No. 2.6e-79;
0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STREET: Virginia COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
    CURRENT APPLICATION NUMBER: US/09/214,095D CURRENT FILING DATE: 1999-07-19 NUMBER OF SEQ ID NOS: 121 SSOFTWARE: Patentin version 3.0 SEQ ID NO 101 LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/554,840 FILING DATE: 07-NOV-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08554840 Patent No. 6001358 GENERAL INFORMATION:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.9%;
Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 836-6620
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BLACK, Amelia APPLICANT: HANNA, Nabil
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                                                                                                                                         TYPE: DNA ORGANISM: Murine
                                                                                                                                                                     ; ORGANISM: MULL:
US-09-214-095D-101
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Sequence 28, Application Us/09332595

Sequence 28, Application Us/09332595

Batent No. 6506383

GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: BADLAN, Eduardo A.

APPLICANT: PADLAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virgin:
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Best Local Similarity 79.4%; Pred. No. 1.9e-78;
Matches 331; Conservative 0; Mismatches 77;
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
'FWACTH: 426 base pairs
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                           LENGTH: 426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION:
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US-09-332-595-28
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US-08-672-345C-89
; Sequence 89, Application US/08672345C
; Sequent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 255.8; DB 4;
Pred. No. 1.9e-78;
0; Mismatches 77;
                                                                                                                                                                                                                                                         ATTORNEY FACENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE DOCKET NUMBER: 012712-127
TELECHONE: (703) 836-6620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PetentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.2%;
79.4%;
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nucleic acid
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Best Local Similarity 79.4
Matches 331; Conservative
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55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC 114
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NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CITY: New York
CITY: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUM-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
TELEFRAMINICATION INFORMATION:
TELEFRAMINICATION DOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 89: SEQUENCE CHARACTERISTICS: LENGTH: 366 base pairs; TYPE: nucleic acid STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: cDNAUS-08-672-345C-89
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Best Local Similarity 84.0°
Matches 300; Conservative
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Search completed: October 24, 2003, 05:50:36 Job time : 60.1212 secs

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BQ922384 AGENCOURT BF582341 G02101173 BI24987 G0229578 BF578272 G02092608 BF580560 G02097363 BF59775 G02095092 BE303370 G01093704 BG963780 G0283871 BF581395 G0102183.

BB859416 BI249884

AA544384 vk33f64.r AA098196 mn86h06.r BG968142 602834777 BF531469 602091586 BF179165 601807413 BF163747 601769849 B1248921 602992521 BF188637 601769849 B1358637 601769849 B1358637 601769849 B1358637 601769849 B1358637 601769849 B1358637 60176989 B1358637 60176923 B135863885440 BY35021 BY350213 BM920469 AGENCOURT BQ708516 AGENCOURT BG685592 602637569

BG686421 602638356 BQ716897 AGENCOURT BG686767 602650737 BU899307 AGENCOURT

AW229937 u045a05.y AW402337 UI-HF-BK0

BQ710683 AGENCOURT BX283435 BX283435 BG397580 602438620

AL552672 AL552672

W402415 UI-HF-BK0

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BI456288 693 bp mRNA linear EST 21-AUG-2001
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAMI1636 row: 1 column: 20
High quality sequence stop: 691.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BF580560
BF59775
BE309330
BG963270
BF585395
BF585395
BF581327
AA544384
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BG968342
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BF179165
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BY3521
AW402602
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BW320469
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AW229337
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BU899307
AL552672
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BX281435
BG397580
AW402415
                                BB859416
BI249884
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      mRNA sequence:
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT:1
BI456288
      B1456288 603172678
BU524092 AGENCOURT
BX007948 BY007948
BG962947 602827932
                                                                                                                                                                                                                 ; Search time 1805.39 Seconds (without alignments) 5532.953 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                              411
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411
1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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Match Length
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329.4
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BY007948 RIKEN full-length enriched, B cells CRL-1702 WEHI 231 cDNA Mus musculus cDNA clone G4D0003J12 5', mRNA sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 502)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Salito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
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/clone_lib="NCI_CGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sal; cloned unidirectionally. Primer: Oligo dT.
Sverage insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Pred. No. 6e-89;
); Mismatches 35;
                                                                                                                                                                                                           1. .963
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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/clone="IMAGE:6530848"
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90.8%;
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Best Local Similarity 90.8
Matches 376; Conservative
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                                                                                   /mol_type="mRNA"
// strain="C57BL/6J"
// db // stref="Laxon:1009"
// clone="INAGE:525131"
// tissue_type="tumor, gross tissue"
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// dev_stage="7 months"
// dev_stage="7 months"
// dev_stage="0100"
// dov_stage="0100"
// dov_stage="0110"
// dov_stage="0100"
// dov_stage="01000"
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// do
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AGENCOURT_10126646 NCI_CGAP_CO24 Mus musculus cDNA clone
IMAGE:6530848 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 4.5e-89;
0; Mismatches 28; ]
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                                                                 organism="Mus musculus"
        location/Qualifiers
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Matches 383; Conservative
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                                                                                                                                                   183 ACTGTCACTGGCTACTCAATCACCCAGTGATTATGCCTGGAACTGGATCCGGCAGTTTCCA
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0; Mismatches 37; Indels
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                      89.5%;
                         Best Local Similarity 89.5
Matches 368; Conservative
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Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani.

L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Fracer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Crimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaj, H.H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchinni, L., McKale, E.D., Mraca, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Vandels, K., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, K.B., Walls, C., Wingher, Y., Taylor, M.S., Teasdale, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Maramura, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Arangisawa, M., Arawa, T., Konno, H., Nakamura, M., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, M., Mayasaki, T., Konno, H., Nakawa, T., Konno, H., Nakawa, Y., Inhia, Y., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Blrney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,K., Ishia,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Saco,K., Shibata,K., Shiraki,T., Tagami
Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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PUBMED
COMMENT
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TITLE

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/organism="Mus musculus"
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/db xref="taxon:10090"
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/note="organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10986 row: o column: 07
High quality sequence stop: 658.
Location/Qualifiers
rce
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 659)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/cell\_type="B cells" /cell\_line="CRL-1702 WEHI 231" /clone\_lib="RIKEN full-length enriched, B cells CRL-1702

80.2%; Score 329.8; DB 13; Length 502;

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WEHI 231 CDNA" 126 c

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Query Match

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Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 483).

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito; M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, H., Tagawa, M., Takaku-Akahira, S., Tanaka, T., Tomaru, Y., Tagawa, M., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Sakaki, Muramatsu, M., and Hayashizaki, Y., RikEN Encyclopedia of Mouse Full-length cDNAB (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB859416 BIKEN full-length enriched, B cells CRL-1702 WEHI 231 CDNA Mus musculus cDNA clone G430007017 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                 Length 770;
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Pred. No. 1.3e-84;
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602834949F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989229 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 770)
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arraped by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11003 row: b column: 14
High quality sequence stop: 766.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                   Gaps
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                                                   DB 12; Length 659;
                                                                                                   41;
                                                   Score 329.4; DB 1
Pred. No. 2.4e-85;
                                                                                                0; Mismatches
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/mol_type="mRNA"
/strain="FVB/N"
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Mus musculus
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                                                   80.1%;
88.7%;
                                                                                                Conservative
                                                                      Best Local Similarity
Matches 370; Conserv
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                                                                                              370;
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                                                      Query Match
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/tissue_type="tumor, gross tissue"
/dev stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not!; Cloned undirectionally. Primer: Oligo dT. Library constructed by Life Technologies, Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Lothar Hen Technologies, Inc.

CIDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:

http://image.llh.gov
Plate: LLAM11375 row: m column: 21

High quality sequence stop: 840.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 909)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 ACTGTCACTGGCTACTCCATCACCAGTGGTTATGCCTGGAACTGGATCCGGCAGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 TCTCTCAAAAGTCGAATCTCTATTACTCGAGACAATCCAAGAAGCAGTTCTTCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 TIGAATICIGIGACTACTGAGGACACACACACATATTACTGTGCAAGAGCACCTCGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 ATGAGAGTGCTGATTCTTTTGTGCCTGTTCACAGCCTTTCCTGGTATCCTGATGTG
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                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 321.2; DB 12; Length 909;
Pred. No. 7.1e-83;
0; Mismatches 48; Indels 3;
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5151932"
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Matches 363; C
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                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequenching pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Eukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahára X., Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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602995987F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151932 5',
mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAGAGTGCTGATTCTTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="B_cells"
/cell_line="CRL-1702 WEHI 231"
/clone_lib="RIKEN full-length enriched, B cells CRL-1702
WEHI 231 CDNA"
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/db_xref="taxon:10090"
/clone="G43007017"
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Location/Qualifiers
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                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information con through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14018 row: m column: 05
High quality sequence stop: 664.
Location/Qualifiers

1. .853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 ACTGTCACTGGCTACTCCATCACCAGTAGTTATAGCTGGAACTGGATCCGGCAGTTTCCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 TCTCTCAAAAGTCGAATCTCTATTACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db.care="taxxon:10090"
/clone="IMAGE:6477196"
/lab_nost="DH10B (Ti phage-resistant)"
/clone lib="WINGI (GAP Co24"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 &b. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
                                                                                                      Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 853)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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0
AGENCOURT 8952317 NCI CGAP_CO24 Mus musculus cDNA clone IMAGE:6477196 5', mRNĀ sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 312.8; DB 13; Length
Pred. No. 2e-80;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                         Mus musculus (house mouse)
                                     BQ922384
BQ922384.1 GI:22337415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.7%;
Matches 326; Conservative (
                                                                                                                                                                                                                    Unpublished
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BF582341
LOCUS
DEFINITION
                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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180
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/lab_host="DH10B (TI phage-resistant)"
/clone lib="NUC CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 CGGCTTCAGGAGTCAGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTGTCCGTCACCTGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 ACTGTCACTGGCTACTCCTTCACCAGTGGTTATTACTGGAACTGGATCCGGCAGTTTCCA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                            Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9814 row: a column: 20
High quality sequence stop: 669.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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86.6%; Pred. No. 2.3e-80;
ative 0; Mismatches 54; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="FVB/N".
BF582341.1 GI:11656053
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                                                                                        Mus musculus
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RESULT

BF582341 910 bp mRNA linear EST 12-DEC-2000 602101173F1 NCI\_CGAP\_CO24 Mus musculus cDNA clone IMAGE:4224283 5',

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BF578272 933 bp mRNA linear EST 12-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db Arge="tayn".
/db Arge="tayn":10090"
/clone="IMAGE:4207320"
/clone="IMAGE:4207320"
/clone=lib="NGT CGAP CC24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 261 c 245 g 192 t
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: .

http://image.llnl.gov
Plate: LLAM9769 row: o column: 01

High quality sequence stop: 655.
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                          385 TAGTTACATCCCCTATGCTTTGGACTATTGGGGTCAAGGAACCTCAGTCACGGTCTCCTC
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Pred. No. 1.3e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Mus musculus
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/strain="FVB/N"
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93.7%;
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Best Local Simi:
Matches 327;
                                                                                                                        445
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                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                       LOCUS
DEFINITION
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ORIGIN
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853 bp mRNA linear EST 17-JUL-2001
6029595978F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5151882 5',
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/note="Organ: mammarY; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies, Investigators
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11375 row: k column: 19
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Pred. No. 8.7e-80;
0; Mismatches 44
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/dev stage="7 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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Location/Qualifiers
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/clone="IMAGE:5151882"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                        Mus musculus (house mouse)
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BI249876.1 GI:14797680
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Best Local Similarity 87.2%;
Matches 367; Conservative
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                                                              mRNA sequence.
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                    LOCUS
DEFINITION
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BF579775 12-DEC-2000 60209592F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4209454 5', BF579775
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281 TCTCTCAAAAGTCGAATCTCTGTTACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:4209454"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NUIC CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 954)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM9775 row: g column: 23
High quality sequence stop: 608.
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Pred. No. 4.3e-74;
0; Mismatches 58; Indels 6;
                                                                                 387
                                          TIGAATICIGIGACIACIGGGGACACGICCACAIAITACIGIGCAAG 347
                                                                  /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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84.6%;
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Matches 352; Conservative
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TITLE
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COMMENT
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/Barin="FURBN"
/db_xref="taxon:10090"
/clone="IMAGE:4217294"
/lab host="BHLOB (Tl phage-resistant)"
/clone=lib="NCI_CGAP_CO24"
/note="Cogan: Colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                          BF580560 866 bp mRNA linear EST 12-DEC-2000 6020097363F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4217294 5', BF580560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM9795 row: n column: 15

High quality sequence stop: 681.

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 ATGAGAGTGCTGATTC-TTTGTGGCTGTTCTCACAGCCTTTCCTGGTATCCTGTCTGATGTG
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                             348
                                                                                                      401
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                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                         BF580560.1 GI:11654272
                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
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TITLE
JOURNAL
COMMENT
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BF580560
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602828311F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983352 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGAAACAAACTGGAGTGGATGGGCTACA-TAAGTTACAGTGGTATCACTACCTACAACC 238
/mol_type="mRNA"
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/bstrain="FVB/N"
/dbxref="taxon:10090"
/clone="IMAGE:4983352"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP_CG24"
/note="Organ: colon", Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
                                                                   TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                            262 TCTCTCAAAAATCGAATCTCCATCACTCGTGACACTCTAAGAACCAGTTTTTCCTGAAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 735)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACTGTCACTGGCTACTCAATCACCAG-TGATCATGCCTGGAGCTGGATCCGGCAGTTTCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Tissue Procurement: deffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Colone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 551.
High quality sequence stop: 551.
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                                                                                                                                                           301 TIGAATICIGIGACTACTGGGGACACGICCACATATIACTGTGCAAG 347
                                                                                                                                                                                    CTGAATTCTGTGACTACTGAGGACACAGCTACATATTACTGTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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Best Local Similarity
Matches 355; Conserv
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                         202
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                                                                                                                                                                                                                                                                   BE309330 741 bp mRNA linear EST 26-OCT-2000 601093704F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3488305 5',
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM8527 row: h column: 02
High quality.sequence stop: 572.
Location/Qualifiers
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                                                                312 Trgaaricrefeacracreaceacaceaceacararrrrerecaagacagarrracrare 371
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to // 11)
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                                                                                                               411
                                                                                                                                        1 (bases 1 to ''1',
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                               361 ACTACGGCTA----TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 279.8; DB 10; Length 741; Pred. No. 8.2e-71; 0; Mismatches 42; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:3488305"
/tissue_type="tumor, gro
/dev_stage="r_months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                            BE309330.1 GI:9167350
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87.9%;
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Best Local Similarity 87.9
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                               mRNA sequence.
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TITLE
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Fv(TU27). Homo sa Variable region an Sequence of the an Anti-traseolide 02 Chimeric antibody Variable region an Fv(TU27). Homo sa

Humanised antibody

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Human, antibody, interleukin-6, receptor, IL-6R, light chain, L, H, heavy chain, variable region, mouse, monoclonal, hybridoma, PM1, plasmid, pPM-k3, pPM-h1, ss.
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AAF76338
AAV99657
AAQ30706
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AAA50159
ABZ21160
AAT39555
AAT69539
AAA30416
AAC9790
ABZ57950
ABZ57950
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ABX03771
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AAT62573
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AAT36663
AAV09801
AAV09803
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ABZ21157
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92JP-0032084
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19-FEB-1992;
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30-MAR-1993
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243.8
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242.4
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 Murine 583 antibod
Antibody 806 varia
MAD 1.4 heavy chai
Monoclonal antibod
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AntiDNP-scFv. Syn
Anti-dinitrophenol
                                                                            October 24, 2003, 02:25:30 ; Search time 204.462 Seconds (without alignments) 5426.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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                                                                                                                                            411
1 ATGAGAGTGCTGATTCTTT......CCTCAGTCACCGTCTCCTCA
            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               2552756 seqs, 1349719017 residues
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Listing first 45 summaries
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AAA74604
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                                                                                                                                                                             IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                 N Geneseq 19Jun03;*
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411 322 316.8 313.4 313.4 297.8 284.6

12645978

Score

8 8

Result

DNA encoding the h DNA encoding the h Nucleotide sequenc Sequence of PCR pr Anti-VHSV single c

Fusion protein L49 Sequence of Clone Fd phage clone seq Humanised variable

Antibody 24-31 hu Murine humanised

DNA encoding 577 heavy Variable heavy 547 heavy Variable heavy cha Anti-human FasL an Monses VH group I (A Monoral antibody DNA encoding the h Humanised antibody Variable heavy sub Antibody 24-31 hum Murine wild-type a DNA encoding the h scfv(1.1ASML) gene VH domain of antibod Monoclonal antibod Monoclonal antibod

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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antibody. It was obtained from total RNA extracted from a SB3 hybridoma by RT-PCR. SB3 is an IgG1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a plezoelectric immunosassying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GGAAACAAACTGGAGTGGATGGGCTACATAAGCTACAGTGGTTTCACTAGCTACAACCCA
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/product= "5B3 antibody heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence encodes the heavy chain variable region of 5B3
                                                                                                                                                                                                                                                                                                                                                                                       Apparatus for detecting small molecules, especially explosives comprises a piezoelectric crystal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 408 BP; 90 A; 108 C; 99 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 322; DB 21;
Pred. No. 3e-91;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3A; 90pp; English
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Best Local Similarity 90.7%;
Matches 343; Conservative 0
                                                                                                                                                                    25-JAN-2000; 2000WO-IL00048.
               /*tag=
                                                                                                                                                                                                                                                                                                  Willner I, Eshhar 2;
                                                                                                                                                                                                                                                                                                                                       2000-524259/47.
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                                                                                         WO200043774-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                           The sequences given in AAQ30755-56 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (LI-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCTCAAAAAGTCGAATCTCTATCACTCGAGACACACCAGGAACAGGTTCTTCCTACAG
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                                                                                                                                               Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 411 BP; 95 A; 114 C; 92 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 411; DB 13;
; Pred. No. 2.7e-119;
0; Mismatches 0;
                                                        Sato K,
                                                                                                                                                                                                                      Disclosure, Page 122-123; 207pp; Japanese.
                                                        Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA74604 standard; cDNA; 408 BP.
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Best Local Similarity 100.0%;
Matches 411; Conservative 0,
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                   춫
                   CHUS ) CHUGAI SEIYAKU
                                                      Jones ST,
                                                                                          WPI; 1992-398882/48
                                                                                                            P-PSDB; AAR28671.
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                                                        Bendig MM,
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RESULT

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is recognizes an epidermal growth factor receptor (EGFR) epitope which is count in tumourigenic. hyperpoliferative or abnormal calls and not detectable in normal cells. The EGFR epitope is located within the region comprising residues 273-501 of EGFR and does not demonstrate any amino comprising residues 273-501 of EGFR and does not demonstrate any amino caid sequence alterations or substitutions from normal EGFR. (I) is capable of binding the de2-7 EGFR at an epitope distinct from the capable of binding the de2-7 EGFR at an epitope distinct from the capable of binding the de2-7 EGFR at an epitope distinct from the command wild-type gene. The binding ambter comprises the VH and VL collypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for the preparation of amplification or reating cancer which is located in or adjacent the community or treating cancer which is located in or adjacent the complexity or treating cancer which is located in or adjacent the complified EGFR or EGFR with high mannose glycosylation; where EGFR is measured by contacting a biological sample from a mammal in which complified EGFR, de2-7EGFR or EGFR with high mannose glycosylation is suspected with (I) unde detecting whether binding has occurred between the EGFR from the sample and the antibody, where the detection of binding indicates that presence or activity of the EGFR in each of the EGFR in measured by contacting capable and the antibody, where the detecting the presence or activity of the EGFR in measured by a useful for detecting cancer in mammals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epidermal growth factor receptor epitope found only in tumorigenic cells, useful for diagnosing, preventing and treating cancer in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel specific binding members, particularly antibodies recognizing
                                                                                                                                                                                                                Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic; monoclonal antibody; mAb 806; antibody therapy; tumour; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ritter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Renner C, Ricture ... Huang H;
                                                                                                                                                                      Antibody 806 variable heavy chain (VH) region encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                       1..54
/*tag= b
55..402
/*tag= c
/rote= "806 VH region"
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                           BP.
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                        ABZ23940 standard; DNA; 402
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                                                                                                                       (first entry)
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existence of a tumour or cancer in the mammal. A pharmaceutical composition comprising (1), and optionally vehicle, carrier or diluent in useful for preventing and/or treating cancer in mammals, especially for treating brain-resident cancers that produce aberrantly expressed EGFR imammals, such as glioblastom, medulloblastoma, meningioma, neoplastic astrocytoma or neoplastic arteriovenous malformations, and malignant neural tumours in mammals. The present sequence represents the mAb 806
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/*tag= a
/product= Monoclonal antibody heavy chain.
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Pred. No. 1.3e-89;
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Best Local Similarity 88.0%;
Matches 345; Conservative
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                                                                                                                                                                    Monoclonal antibodies which inhibit type II phospholipase A2 are useful in the treatment of myocardial infarction, cerebral infarction, acute kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult respiratory distress syndrome and colitis. The antibodies were generated by immunising Balb/C mice with recombinant human type II phospholipase A2. Spleen cells from the mice were fused with mouse myeloma P3U1 (P3x63Ag3.U1) and the hybridomas obtained were screened for phospholipase A2 inhibitory activity. Active clones were isolated including 12H5, 1.4 and 10.1. These were cultured and the antibody isolated from the culture
                                                                                                                                                                                                                                                                                                supernatant by precipitation with ammonium sulphate and purification on a column of protein A-Sepharose CL4B. Because the antibody acts on the primate and mouse forms of enzyme as well as human it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody 1.4 heavy chain against type II phospholipase A2
                                                                                                            Monoclonal antibody inhibiting type II phospholipase A2 activity for treatment of myocardial and cerebral infarction
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                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.3%; Score 313.4; DB 17; Best Local Similarity 86.9%; Pred. No. 1.5e-88; Matches 357; Conservative 0; Mismatches 51;
                                              ٠<u>;</u>
                                                 Yasunaga
                                                                                                                                                                                                                                                                                                                                      particularly suitable for preclinical testing
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                                                                                                                                               Example 6; Figure 11; 69pp; Japanese.
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                                                 Takasaki J,
                        (YAMA ) YAMANOUCHI PHARM CO LTD
94JP-0340006
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                                                 Masuho
                                                                        WPI; 1996-333946/33
                                                                                     P-PSDB; AAW01144
29-DEC-1994;
                                                 Kawauchi Y,
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The present sequence encodes the monoclonal antibody 1.4 heavy chain against type II phospholipase A2, from the present invention. The present invention describes a novel method for the amelioration of kidney disorders (such as acute renal failure) associated with the administration of cisplatin for the treatment of cancer. The method comprises treatment with a monoclonal antibody which inhibits the activity of type II phospholipase A2 (particularly of type II phospholipase A2 (particularly of type II phospholipase A2, with a protein or peptide possessing the same inhibitory activity and contening a part of the antibody sequence. Preferably the antibody also inhibits the activity of ape and/or mouse type II phospholipase A2, and has the ability to release type II phospholipase A2, bound to a cell membrane. Three specific monoclonal antibodies having these properties which can be used are 12H5, 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-529 and FERM BP-5297, respectively. The method can be used for cisplatin administration, and therefore allowing more efficient use of the content of the content agent, e.g. by allowing an increased dosage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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cisplatin;
ds.
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                                                                                                                                                                                        1..408
/*tag= a
/product= "monoclonal antibody 1.4 heavy chain"
/notes "no stop codon given"
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Pred. No. 1.5e-88;
0; Mismatches 51; Indels 3;
   Monoclonal antibody; type II phospholipase A2; inhibition; amelioration; kidney disorder; nephrotoxicity; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 408 BP; 96 A; 108 C; 95 G; 109 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masuho Y,
                                                                                                                                                          location/Qualifiers
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86.9%; Pred
0; N
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96JP-0167286.
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Best Local Similarity 86.9
Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawauchi Y,
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357;

Length

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TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG 300
                                                                                                    TIGAATICIGIGACIACIGGGACACGICCACAIAITACIGIGCAAGAICCCIAGCICGG 360
                                                                                                                               TTGACTTCTGTGACTACTGGGGCACACACATATTACTGTACAAGAGACTTGG---AC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the heavy chain variable region for monoclonal antibody (MAb) 13D10, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from hydridoma cells from mouse spleen cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials
                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as
                                                                                                                                                             411
                                                                                                                                                                                                                                                                                                                                                  Lead binding MAb 13D10 heavy chain variable region encoding cDNA
                                                                                                                                                                             GCCTGGTACTTCGATGTTTGGGGCGCAGGGACAACGGTCACCGTCTCCTCA 408
                                                                                                                                                           ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
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/*tag= a
/note= "no stop
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95US-0462798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043140/04.
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05-JUN-1995;
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Sequence 357 BP; 91 A; 100 C; 79 G; 87 T; 0 other;

for electronic components.

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                                                                                                                         115 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The anti-hapten dinitrophenol single chain antibody (anti-DNP scFv) encoded by this sequence is used as a targeting peptide (TP), which is fused to the envelope protein of a retroviral vector. When the TP is fused to the envelope protein, it replaces or disrupts the natural receptor binding site. By using a TP that recognises a cell surface antigen, the retroviral vectors containing TP's can be used in a cell type specific method for introducing genes into cells. These retroviral vectors can be used in the gene therapy of human genetic diseases including, adenosine deaminase (ADA) deficiency, and in clinical trials
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                                                                                                                                                                                                                                                                                                                                                                                                           301 AACTACCCGTGGTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 357
                                                                                                                                                                                                            AACCCATCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTC
                                                                                                                                                                                                                                                                       Antibody; scFv; targeting peptide; retroviral vector; gene therapy; adenosine deaminase deficiency; ADA; cancer; hapten dinitrophenol; ss.
                                                              GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
                                                                                           GARGIGCAGCITCAGGAGICGGGACCIGGCGAGAAACCITCTCAGICTCTGTCCCTC
                                                                                                                                                                                        Gaps
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                                Indels
Score 297.8; DB 18;
Pred. No. 1.2e-83;
0; Mismatches 37;
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 Query Match 72.5%;
Best Local Similarity 89.6%;
Matches 320; Conservative
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Example, Fig 3, 45pp; English
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to cure cancer. A wild type envelope can be used in addition to the altered vector, and will act as a helper molecule. The helper function enhances the infection of cells by the retroviral vector.
                                                                                                                                                                                                                                                                                        280 TCTCTCAAAAGTCGAATCTCCATCACTCGAGACACATCCAAGAACCAGTACTACCTGCAG
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                                                                                                     1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGATGTG
                                                                                                                          CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC
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                                                                                                                                                                                                             163 TCTGTCACTGGCGACTCCATCACCAGTGGTTA---CTGGAACTGGATCCGGAAATTCCCA
                                                                                                                                                                                                                                 GGAAACAAACTGGAGTGGGATGGGCTACATAAGTTACAGTGGTATCACTACCAACCCA
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                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retroviral vector; Spleen Necrosis Virus; SNV; antibody-envelope fusion protein; retroviral envelope protein; gene therapy; antigen binding site; single chain antibody; scPv; dinitrophenol; DNP; cell specific gene transfer; ds.
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                                                             Length 836;
                                                                                                                                                                                                                                                                                                                                                                        361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
                                                           Score 284.6; DB 16; Length
Pred. No. 2.4e-79;
0; Mismatches 59; Indels
                                       Sequence 836 BP; 219 A; 198 C; 213 G; 206 T; 0 other;
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                                                           / Match 69.2%;
Local Similarity 84.2%;
hes 346; Conservative (
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The patent discloses a novel retroviral vector, particularly Spleen
Necrosis Virus (SNV) vector, having target cell specificity. The vector
has a targetting envelope which is a chimeric protein consisting of an
antigen binding site of an antibody (e.g. anti-DNP-SGFV) or another
peptide that binds to a specific cell surface protein, fused to the
carboxy terminal part of the retroviral envelope protein. The presence
of the wild type envelope protein serves as a helper molecule to
improve or supplement a functional membrane fusion domain. The
carboxing site replaces the natural viral receptor binding site.
The retroviral vector is used for cell specific gene transfer,
especially in gene therapy. The invention overcomes the restricted host
cange limitation of retroviral vectors. The present sequence is a gene
encoding single chain antibody (serv) against hapten dintrophenol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 caderireaddacteaddaceradecerdaaacericerdacrererererererere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 rereresereses recareaceas recentations and recession recent r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTCTGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of the single chain antibody gene (scFv) against the hapten dinitrophenol (anti-DNP-scFv).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector; antigen binding site; antibody; envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 284.6; DB 21; Length
Pred. No. 2.4e-79;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 836 BP, 219 A, 198 C; 213 G; 206 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targetting envelope of retroviral vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.2%;
Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         836
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGAGAGTGCTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ66698 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroviral vector; anti
dinitrophenol; DNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9412626-A1
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21-DEC-1994
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The present invention describes the detection, in a subject, of antibodies (Ab) that recognise an integrin (I) when bound to its agonist or antagonist (II) comprises forming a (I)-(II) complex, incubating this with source of Ab and detecting Ab that binds.

The comprises forming that the constant of the complex of (II) constant of the complex of (II) are used as positive controls in the method. The present sequence represents a specifically claimed chimeric antibody heavy chain nucleotide sequence.

It is a subject to the complex of (II) and a particular (II) are used as positive controls in the method. The present sequence represents a specifically claimed chimeric antibody heavy chain nucleotide sequence. (II) are used to treat thromboenholic disorders, e.g. anging a pectoris, myocardial infarction, stroke, or pulmonary embolism, but may cause thromboeytopenia or other complications, in some patients. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCTCAAAAGTCGAATCTCTATCACTCGAGACAACAAGAACCAGTTCTTCCTACAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provides a more sensitive detection of DDAb and can be made specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.B. The sequence given in the specification is stated as being 1420 nucleotides long but the sequence given is only 1200 nucleotides long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ATGAAAGTGTTGAGTCTGTTGTACCTGTTGACAGCCATTCCTGGTATCCTGTCTGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCTTCAGGAGTCAGGACCTGGCCTCGTGAAACCTTCTCAGTCTCTGTCTCTCACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and optimizing treatment of thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting antibodies that recognize complexes of integrin with its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Score 281.2; DB 20; Length 1200;
llarity 81.6%; Pred. No. 3.2e-78;
Conservative 0; Mismatches 73; Indels 3;
thrombocytopenia; thromboembolic disorder; angina pectoris; myocardial infarction; stroke; pulmonary embolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1200 BP; 284 A; 368 C; 303 G; 245 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 Dicker IB,
O'Neil KT,
                                                                                                                                                                                                                                                                                                                                                              A, Burn TC,
Kochie JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 46; Page 101; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulator, for monitoring and opt
conditions with these modulators
                                                                                                                                                                                                                             99WO-US01640.
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                                                                                                                                                                                                                                                                                                                   (DUPO ) DU PONT PHARM CO.
                                                                Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                    Hollis JM,
                                                                                                                                                                                                                                                                                                                                                                   Breth
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-458734/38.
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es 338; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Billheimer JT
                                                                                                                                                                                                                             27-JAN-1999;
                                                                                                                                                                                                                                                                           27-JAN-1998;
                                                                                                                                   W09938014-A1
                                                                                                                                                                                29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                        Hollis GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGATTAAACTTGAGTACATGGGGTACATAAGCTACAGTGGTAGCACTTACTACAATCCA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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                                                                                                                                                                                                                                                                                                                                                              The genes coding for the heavy and light chain of an antibody against DNP were provided by Dr Ogawa of Scripps Clinic, La Jolla, Ca. The genes were sequenced and published (Riley et al. 1986).

Using PCR a single chain antibody gene was constructed using the signal peptide against DNP. The PCR product was cloned into the Smal site of pBluescript. DNA sequencing confirmed the successful combination of the two gene segments coding for the variable regions of the annigen binding peptide. The complete sequence of the anti-(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTATGCTATGGAGTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                Retroviral vector with target cell specificity - used for gene therapy by direct injection into a patients bloodstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric; drug dependent antibody; DDAB; integrin; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.9%; Score 283; DB 15; Length 836; Best Local Similarity 83.9%; Pred. No. 7.5e-79; Matches 345; Conservative 0; Mismatches 60; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAGAGTGCTGATTCTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 836 BP; 218 A; 198 C; 213 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric antibody heavy chain nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                      Example, Fig 3; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX90424 standard; DNA; 1200
                   93WO-US11258
                                                              92US-0979619
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                                                                                                           NEW JERSEY
                                                                                                                                                                                                 WPI; 1994-200255/24.
                                                              20-NOV-1992;
                                                                                                        (UYNE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999
                                                                                                                                                        Dornburg RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The constructed plasmids pFv (TU27)-DE and pFv (TU25)-DE which express polypeptides consisting only of the V regions were purified and sequenced. The polypeptides are capable of binding to the beta chain of IL-2 receptor and of inhibiting the binding of IL-2 to the receptor. They are useful as immunomodulators and immunosuppressants, e.g. to prevent graft rejection or to treat inflammatory allergic and autoimmune diseases, or leukemia. Unlike cyclosporin etc. they are both effective and safe. (Updated on 25-MAR-2003 to correct PN field.)
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Pred. No. 1.1e-77;
0; Mismatches 38; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
heavy; beta; chain; interleukin; II-2; receptor; inhibition;
immunomodulator; immunosuppressant; graft rejection; allergy;
autoimmune disease; leukemia; cyclosporin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide(s) which bind H chain of human IL-2 receptors treating inflammatory, allergic and auto-immune disorders, leukaemias etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 720 BP; 186 A; 188 C; 170 G; 176 T; 0 other;
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ilarity 88.5%;
Conservative C
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(first entry)
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P-PSDB; AAR34510.
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20-AUG-1993
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Matches 315;
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     TCTCTCAAAAATCGAATCTCCATCACTCGTGACACATCTAAGAACCAGTTTTTCCTGAAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ACCTGCTCTGTCACTGGCTACTCCATCACCAGTGGTTATTACTGGAACTGGATCCGGCAG 120
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                                        TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAG---CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ACCTGCACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAG
                                                                        314 TIGAATICIGIGACTACTGAGGACACAGCTACATATTACTGIGCAAGAGATAGAGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTC
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partial
product= "Variable region anti-bisphenol A antibody
                                                                                                                             374 GACCACGGGGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTTGTG 427
                                                                                                                                                                                                                                                                                                                                                                             anti-bisphenol A; antibody; murine; heavy chain;
                                                                                                             358 CGGACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                            Variable region anti-bisphenol A antibody chain coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for the preparation of recombinant protein.
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llarity 86.6%;
Conservative
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P-PSDB; ABB98906.
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es 309; Conserv
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11-NOV-1991;
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28-DEC-1992
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  368 AGGTCAAACTCGAGGAGTCTGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTGTCCCTCA 427
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                                                CCTGCACTGTCACTGGCTACTCACCCAGTGATCATGCCTGGAGCTGGATCCGGCAGT
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chain #1"
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light chain; gene; ds.
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P-PSDB; ABB98905.
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DB 25; Length 357;

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Query Match

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           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the anti-urokinase antibody kappa variable region (\mathsf{VK}) \mathsf{CDNA}.
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                                GATGTGCAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric monoclonal antibody; anti-urokinase antibody; PCR; antithrombotic agent; myocardial infarction therapy; ss.
           Indels
Pred. No. 4.2e-77;
0; Mismatches 50;
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/*tag= d
/label= 5'VH1 primer
340..371
/*tag= e
/label= 3'mVH primer
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/*tag= f
/label= JH01 primer
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10.378
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1.27
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/label= VH01 p
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(first entry)
          307; Conservative
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completed: October 24, 2003, 03:57:08
le : 205.462 secs
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                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                antibody-producing hybridoma Wil-a calls. Using this poly(A) RNA as antibody-producing hybridoma UK1-3 calls. Using this poly(A) RNA as a template, an anti-urokinase antibody VK cDNA was amplified with the mC-kappa primer as primer for first strand sysnichesis, and the 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The amplified fragment was restriction disested and ligated into a restriction fragment of pTB1423 to give an anti-urokinase antibody VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is given in AAQ25667. The cDNA is a functional VK gene. The sequence of (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                      Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 378 BP; 92 A; 100 C; 91 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                    Poly(A) + RNA was prepd. from mouse anti-urokinase
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                        Tada
                                                                                                                                                                                                                                     Example; Figure 15; 87pp; English
                        Watanabe T,
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Best Local Similarity 86.4%;
Matches 317; Conservative
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                        Iwasa S,
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304 AATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGGACT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immobilised binding proteins for specific cpds - obtd. by expressing chimeric proteins comprising the binding protein and cell wall-anchoring protein in host cells
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Pred. No. 1.2e-75;
0; Mismatches 37; Indels 6;
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PCR; amplification; primer; light chain; hybridoma; scFv; single chain antibody; monoclonal antibody; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klis FM,
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243 180

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October 24, 2003, 02:40:25 ; Search time 1641.41 Seconds (without alignments) 10243.574 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 (bases 1 to 411)
Tsuchiya, M., Sato, K., Bendig, M.Margaret., Jones, S.Tarran. and Saldanha, J.William.
Seshaped human to human interleukin-6 receptor
Patent: US 5795965-A 30 18-AUG-1998, TITLE JOURNAL Pred. No. is the number of results predicted by chance to have a

Unclassified.

REFERENCE AUTHORS

M19899 Mouse Ig re
D12726 Mus musculu
M13050 Mouse Ig re
AR108677 Sequence
D12734 Mus musculu
M19893 Mouse Ig re
M15231 Mouse Ig re
M154137 Mus musculu
M19895 Mouse Ig re
M19775 Mouse Ig ac
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M17283 Mouse Ig ac
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L20957 Mus musculu
L20962 Mus musculu
U05284 Mus musculu
AX027688 Sequence
U65534 Mus musculu
U6553 Synthetic M E05894 DNA sequenc U16690 Mus musculu AJ252270 Mus muscu AF006832 Mus muscu PAT 05-DEC-1998 BD011353 Chimeric E05354 DNA encodin E05420 cDNA sequen E43823 Chimeric an X05878 Mouse mRNA L20961 Mus musculu D12728 Mus musculu BD174581 Gene enco BC002091 Mus muscu Y16457 Mus musculu AF165121 Mus muscu 3D174580 Gene enco AR024276 Sequence AR045129 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description linear DNA Sequence 30 from patent US 5795965. AR024276 AR024276.1 GI:3977570 ALIGNMENTS SUMMARIES MUSIGHAAC MUSOHP1.38G MUSIGHGK MUSCHPTD7G MUSCHPAO MUSCHAM MUSCHNOH MUSCHNOH MUSCHXY MUSCHXY MUSIGHNUL1 MUSOHP57G MUSOHP1E9G E43823 MMIGVHR2 MUSIGHDQA AX236250 MMU65534 SCU65536 MUSIGHXX MMU291693 MMU223544 BD174581 BC002091 E05894 BD174580 MMY16457 AR024276 AR045129 BD011353 E05354 E05420 AR141689 AR287724 AR108677 T 0 00000 10 DB Query Match Length 4432 3358 3358 3357 4402 3351 351 358 351 . Unknown. Unknown 283.4 280.4 280.2 279.8 279.2 278.2 278 277.6 Score 335.4 332.2 330.2 329.4 327.8 302.6 298.4 297.8 297.8 297.4 294.6 293.4 292.6 291.8 289 288.2 286.2 319. 312. DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AR024276 LOCUS Result No.

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360 360

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Chimeric antibody against human interleukin-6 receptor.
BD011353
BD011353.1 GI:18639726
JP 2001083151-A/27.
ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA 180
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THOSE WILLIAM SALDANHA
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PC C07K19/00,C12N15/09,(C12N15/09,C12R1:91),A61K37/02,C12N15/00,

PC (C12N15/00,C12R1:91)

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Location/Qualifiers

FT mat_peptide (55). (411).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 411)
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/organism="Mus sp."
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/db xref="taxon:10095"
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Reshaped human antibody to human interleukin-6 receptor Patent: US 5817790-A 30 06-OCT-1998;
Location/Qualifiers
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25-APR-1991 JP 1991095476
TSUCHIYA MASAYUKI, SATO ISAO, MEARII MAAGARETSUTO BENDEITSUGU,
SUTEIIBUN TARRN JIYOONZU
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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100.0%; Pred. No. 4.7e-128;
ive 0; Mismatches 0;
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/mol type="genomic RNA"
/db_xref="taxon:10095"
_114 c 92 g 11
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mat_peptide 55. .411.
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JP 1993227970-A/4.
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/strain="ML-05"
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Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H.
Chimeric antibody against human interleukin-6 receptor
Patent: JP 200116391-A 27 25-APR-2000;
CHUGAI PHARMACEUT CO LTD
S Mus sp. (mouse)
PN JP 2000116391-A/27
PD 25-APR-2000
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C12N15/09,C07K16/18,C07K16/26,C07K19/00,C12N5/10,C12P21/08,
C12N15/00,
                                                                             61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCTCTGCCTCACCTGC
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301 TIGAATICTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG
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larity 100.0%; Pred. No. 4.7e-128;
Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
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RESULT E43823

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/db xref="caxon:10090"
/cell type="hybridoma"
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/codon_start=1
/product="Vh gene product"
/protein_id="CAA29302.1"
/db xref="G1:5227"
/translation="MRVLILLCLVAFPGILSDVQLQESGPDLVKPSQSLSLTCTVTG
YSITSGYTWHWINGPEROKILEWMAYTHYSGNTDFNPSLKSRISITRDTSKNOFFLQLN
SVTAEDTATYYCARGYGNYYAMDYWGQGTSVTVSSAKTTPPSVYPLA"
MMIGVHR2 450 bp mRNA linear ROD 07-MAY-1992
Mouse mRNA for immunoglobulin heavy chain variable region.
X05878 Y00330
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 450)
Grant, F.J., Levin, S.D., Gilbert, T. and Kindsvogel, W.
Improved RNA sequencing method to determine immunoglobulin mRNA
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constant region; Ig heavy chain; variable region
Mus musculus (house mouse)
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/note="constant region (AA 138-149)"
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/note="variable region (AA 1-137)"
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/product="immunoglobulin heavy chain"
/protein_id="AAB01613.1"
/do xref="cd:309342.1"
/tab.xref="cd:309342.1"
/trablation="MRVIILL"
/trablatwwwlRQFPEGDKLEWMGYTTYSGSTSNNPSLKSRISITRDTSKNQFFLQLN
SVTTEDTATYYCARLSVGLRLDYWGQGTTLTVSS"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 2.3e-102;
0; Mismatches 31;
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Patent: WO 0164749-A 108 07-SEP-2001;
Idec Pharmaceuticals Corporation (US)
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AX236250
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/db_xref="taxon:10095"
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91.78;
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368. .408
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Matches 377; Conservative
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Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S.
Structural profile of idiotype, anti-idiotype and
anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds
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Iwasaki,Y., Takabatake,H., Monestier,M. and Ferrone,S.
Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb
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/cell_type="hybridoma"
/tissue_type="hyperimmunized_spleen"
/dev_stage="adult"
1. .>408
/standard_name="anti-HLA-DQ3 monoclo
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95045941
           Pred. No. 4.9e-103;
0; Mismatches 46;
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db_xref="taxon:10090"
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"mol type="mRNA"
'strain="BALB/c"
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         88.88;
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SVTTEDTATYYCAREAYGYDVGYFDYWGQGTTLTVSSAS"
116 c 99 g 114 t

      MUS musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.

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Mus musculus (house mouse)
Mus musculus
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Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Ferrone,S. Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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Idiotypic diversity and variable region gene usage by mouse
anti-HLA-DQ3 mAb
                                                                                                                                                                                                             ; 9
                                                                                                                                                   Length 423;
                                                                                                                                                                                                             Indels
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95045941
                                                                                                                                                   Score 332.2; DB 6;
Pred. No. 2.9e-101;
0; Mismatches 33;
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|mol_type="mRNA"
|strain="BALB/c"
|sub_species="domesticus"
|db_xref="axon:10090"
|sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 42 (2), 90-100 (1995)
95331832
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                                                                                                                                                      80.8%;
90.6%;
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 378; Conserv
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ORGANISM
                                                             BASE COUNT
ORIGIN
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MUSIGHDQC
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VERSION
KEYWORDS
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TITLE
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PUBMED
FEATURES
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PUBMED
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Mus musculus Ig rearranged H-chain mRNA V-region, 5' end of cds.
L20962
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Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S. Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic
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/cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
/dev_stage="adult"
1. .>402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACTACGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
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95045941
7957578
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 330.2; DB 10,
Pred, No. 1.4e-100;
0; Mismatches 33;
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Best Local Similarity 89.8%;
Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                  349. 359
360. 402
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44. .348
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YSITSDYAWNNIRQPGIKLEWMGFISYSGSTSYNBSLESRISVTRDTSKNQFFLQLY
SVTTEDTATYYCANMITTSAYWFDVWGAGTTVTVSS"
                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 417)
Tempest, P.R.
Direct Submission
Submitted (21-AAN-1994) Philip R. Tempest, ICOS Corporation, 22021
20th Ave SE, Bothell, WA 98021, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CAGCTTCAGGAGTCGGGACCTGGCCGTGAAACCTTCTCAGTCTGTGTCCTCTCACCTGC 120
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                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 41)
Tempes; P.R., White, P., Buttle, M., Carr, F.J. and Harris, W.J. Identification of framework residues required to restore antigen binding during reshaping of a monoclonal antibody against the glycoprotein gB of human cytomegalovirus
Int. J. Biol. Macromol. 17 (1), 37-42 (1995)
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/evidence=experimental
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                                                   Mus musculus (house mouse)
Mus musculus
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55. .417
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     GI:463457
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Matches 369; Conserv
     U05284.1
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ORIGIN
                                                                          ORGANISM
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TITLE
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AUTHORS
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/product = 1,1munoglobulin heavy chain"
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/db_xref="G1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGAGTGCTGATTCTTTTTGTGGCTGTTCACAGCCTTTCCTGGTATCCTGTTGTGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                    Iwaski,Y., Takabatake,H., Monestier,M. and Ferrone,S. Idiotypic diversity and variable region gene usage by mouse anti-HLA-DQ3 mAb mannogenetics 42 (2), 90-100 (1995) 9531832 760710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard_name="anti-HLA-DQ3 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Pred. No. 2.5e-100;
0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                        /cell_type="hybridoma"
/tissue_type="hyperimmunized spleen"
/dev_stage="adult"
1. >399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                sub_species="domesticus"
db_xref="taxon:10090"
                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 94.2%;
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                      sex="male"
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     (bases 1 to 399)
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44. .348
349. .361
362. .399
a. 107 c
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                                                                                                                                                                                                      source
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LOCUS
DEFINITION
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REFERENCE
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TITLE
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MEDLINE
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                                                                                                                                                                            FEATURES
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/codon_start=1
/product="immunoglobulin gamma 1 chain"
/product="immunoglobulin gamma 1 chain"
/product="immunoglobulin gamma 1 chain"
/product="immunoglobulin gamma 1 chain"
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/translation="MRVLILLMLFTAFPGILSDVQLQESGPGLVKPSQSLSLTTCTVTG
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HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPRKPVLTITLTFRKTCNVDI
SKDDPEVQEWFVDDVEVHTAQTOPREGERSWSYFIFPRNYGNDITTTLTFRKTCVVVDI
SKDDPEVQEWFVDDVEVHTAQTOPREGERSWSTRFRSVSELPIMHQDWLNGKEFKCRVN
SAAFPAPIEKTISKTRGRPAPQVYTIPPPREGMAKDKVSLTCMTDFFPEDITUEWQ
WNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKS
                                                                                                                                                                                                           2 (bases 1 to 1517)
Siao, XW. and Frenkel, M.J.
Direct Submissel, Biomolecular Engineering, CSIRO, 343 Royal
Barade, Parkville, Victoria 3052, Australia
Location/Qualifiers
                                                                                             Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCU65536 825 bp mRNA linear SYN 07-MAR-
Synthetic Mus musculus single chain Fv antibody precursor mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCCTGGAGCTGGATCCGGCAGTTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 321; DB 10;
Pred. No. 2.1e-97;
0; Mismatches 15;
                                                                                         Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurogna
1 (bases 1 to 1517)
Xiao,X.W. and Frenkel,M.J.
Full-length immunoglobulin gamma chain
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/cell_line="hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                               1 line="hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   מ
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                                                         Mus musculus (house mouse)
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95.7%;
                   GI:1513181
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U65534.1
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Best Local
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SCU65536
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                 source
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ORIGIN
                                                                           ORGANISM
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                 REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                             FEATURES
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Mus musculus immunoglobulin gamma 1 chain mRNA, complete cds.
                                                                                                                                                                                                                                                   PAT 16-SEP-2000
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 TCTCTCGAAAGTCGAATCTCTGTCACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG 300
                                       TTGAATTCTGTGACTACTGGGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
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                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eshhar, Z. and Willner, I. Detection of small molecules by use of a piezoelectric sensor Patent: WO 043774-A 5 27-JUL-2000; YISSUM RES DEV CO (IL); ESHHAR ZELIG (IL); WILLNER ITAMAR (IL) YEDA RES & DEV (IL)
                                                                                                                 361 ACTAC-----GGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411
                                                                                                                                       TCTGCTTACTGGTATTTCGATGTCTGGGGCGCAGGACCACGGTCACCGTCTCCTCA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TCTCTCAGAAGTCGAATCTCTTTCACTCGAGACACATCCAAGAACCAGTTCTTCCTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAGAACCAGTTCTTCCTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGCTTCAGGAGTCGGGACCTGTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAACAAACTGGAGTGGGTTACATAAGTTACAGTGGTATCACTACCAACCCA
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                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 6;
8.4e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 322; DB
Pred. No. 8.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                 AX027688 408 bp
Seguence 5 from Patent WO0043774.
AX027688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
108 c 99 g 11
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                                                                                                                                                                                                                                                                                                           AX027688.1 GI:10188558
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Best Local Similarity 90.7%;
Matches 343; Conservative (
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
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RESULT 14

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GSGTDPTLKISRVBABDLGVYYCFQGSHVPFTFGAGTKLELKDYKDDDDK"
                                                                                       Aguinett Concerned attitions and Frenkel, M.J.
Xiao, X.W. and Frenkel, M.J.
Single chain Fv with signal sequence
Unpublished
2 (bases 1 to 825)
Xiao, X.W. and Frenkel, M.J.
Xiao, X.W. and Frenkel, M.J.
Sirect Submission
Submitted (30-JUL-1996) Biomolecular Engineering, CSIRO, 343 Royal Parade, Parkville, Victoria 3052, Australia
Location/Qualifiers
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Pred. No. 6.9e-97;
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organism="Mus musculus"
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Search completed: October 24, 2003, 04:50:11 Job time : 1643.91 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Searched:	OM nucleic - nucleic search, using sw model  Run on: October 24, 2003, 02:40:25 ; Search time 1521.59 Seconds  (without alignments) 10243.574 Million cell updates/sec  Title: US-09-114-285A-28  Perfect score: 381 Sequence: 1 ATGGTGCTCAGGTTGGACCAAGCTGGAATAAAT 381  Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2888711 seds, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0 Maximum DB seq length: 21	Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:\*

GenEmbl:\*

1: gb ba:\*
2: gb\_htg:\*
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11: gb\_crs:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR024275 Sequence AR045128 Sequence BD011352 Chimeric E05553 DNA encodin E49822 Chimeric an E05419 cDNA sequen S50261 Ig VL=anti- 133380 Sequence 1 L55316 Mus musculu M60019 Muse Ig ka U16689 Mus musculu AR045496 Mus muscul AR016717 Sequence U05217 Mus muscul AR46770 Mus muscul BC015292 Mus muscul BC015292 Mus muscul	A51499 Sequence 1 AR08577 Sequence AR024279 Sequence AR04513.2 Sequence BD011356 Chimeric E05375 DNA encodin E43826 Chimeric an	M17160 Mouse 1g ka AR301133 Sequence AY081858 Mus muscu E06647 CDNA encodi M27793 Mouse 1g ka M60020 Mouse 1g ka BC027418 Mus muscu AR002741 Sequence AR032023 Sequence AR03819 Sequence AR03819 Sequence AR048519 Sequence AR05888 CDNA encodi S63022 anti-gangli AR050865 Sequence E05888 CDNA encodi S63022 anti-gangli X5044 M. musculus X55044 M. musculus X55044 M. musculus X55041 M. musculus	DNA linear PAT 05-DEC-1998 aret., Jones, S. Tarran. and i
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Result No. Sco.	11 35 35 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	- 8 0 0 0 1 0 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0	4	RESULT 1 AR024275 LOCUS DEFINITION ACCESSION VERGION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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Chimeric antibody against human interleukin-6 receptor.
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PC G01N33/53, A61K39/00, A61K39/395, A61R39/395, A61P35/00, PC
G01N33/577/CO7K16/28,
PC C07K19/00, C12XN15/09, (C12XN15/09, C12XN15/00, C
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Bukaryota, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (Dases 1 to 381)

Tsuchiya, M., Sato, K., Bendigu, M.M., Jones, S.T. and Saldanha, H.W.

Chimeric antibody, against human interleukin-6 receptor

Patent: JP 2001083151-A 26 30-MAR-2001;

CHUGAI PHARMACEUTICAL CO LTD
181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                                                                                241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGGAA
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JP 2001083151-A/26
30-MAR-2001
28-JUL-2000 JP 2000229748
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1 (bases 1 to 381)
Tsuchiya,M., Sato,K., Bendig,M.Margaret., Jones,S.Tarran. and Saldanha,J.Vailliam.
Reshaped human antibody to human interleukin-6 receptor Patent: US 5817790-A 28 06-OCT-1998;
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                                                                                                                                                          Length 381;
                                                                                                                                                        Score 381; DB 6; Length 3; Pred. No. 7.2e-114; 0; Mismatches 0; Indels
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Tsuchiya,M., Sato,I., Margaret,B.M., Taren,J.S. and William,S.H. Thimeric antibody against human interleukin-6 receptor Patent: JP 2000116391-A 26 25-APR-2000; CHUGAI PHARMACEUT CO LTD
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Chimeric antibody against human interleukin-6 receptor.
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/organism="Mus sp."
/mol_type="genomic DNA"
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mat_peptide (61)..(381)
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25-APR-2000
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Light Muridae; Murinae; Mus
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Nus ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
Nus Sp. (mouse)
NN JP 193227970-A3 07-SEP-1993;
ND 07-SEP-1993
PP 19-FEB-1992
PP 19-FEB-1992 JP 1992032084
PI TSUCHIYA MASAYUKI, SATO 16A0, MEARII MAAGARETSUTO BENDEITSUGU, PI SUTEIIBUN TAREN JIYOONZU, HOSE UIRIAMU SARUDANA PC
C12N15/10,
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CC topology: Linear;
CC *source: clone=pPM-k3;
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DNA encoding V region of L chain of mouse monoclonal antibody
against human interleukin-6 receptor.
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mat_peptide 61. .381.
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JP 1993227970-A/3.
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/gene="Ig VL"
/note="This sequence comes from Fig. 1a"
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/db_xref="GI:260762"
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ASQDINNYLSWYQQFRDGTVKLLIYTTSRLHSGVPSRFSGSGSGTDYSLTITNLEQED
VATYFCQQGRTLPYTFGGGTKLEIK"
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191 bp mRNA linear ROD 08-MAY-1993

19 VL=anti-CD4 mAb M-T151 variable region light chain {J2, chimeric antibody} [mice, hybridoma cells, mRNA Partial, 381 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 381)
Weissenhorn, W., Scheuer, W., Kaluza, B., Schwirzke, M., Reiter, C., Plieger, D., Lenz, H., Waiss, E.H., Raber, E.P., Riethmuller, G. et, al. Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor
Gene 121 (2), 271-278 (1992)
                                                                                                                                                                                            /gene="Ig VL"
/note="anti-CD4 mAb M-T151 variable region light chain"
61 GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                          181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                                                                                                                  121 ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                          GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                       GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .381
/organism="Mus sp."
/mol type="mRNA"
/db_xref="taxon:10095"
1. .381
/partial
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/partial
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AUTHORS
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Tauchiya, M., Sato, I., Mearii, M.B. and Suteibun, T.J.

DNA CAPABLE OF CODING VARIABLE REGION OF MURINE MONOCLONAL ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR

AL TO HUMAN INTERLEUKIN-6 RECEPTOR

PATENTIAL JP 1993216966-A 26 17-SEP-1993;
CHUGAI PHARMACEUT CO LTD

OS (mouse)

PR 25-APR-1991 JP 19911095476

PI 7-SEP-1993

PR 25-APR-1991 JP 19911095476

PI SUTEIIBUN TARRN JIVOONZU

PC CI2N15/13/C12P21/08;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC **BOUTCE: cell linear;
CC **BOUTCE: cell line=PM1;
CC **BOUTCE: clone=pPM-k3;
FH Key

FT mat_peptide 61..387

FT mat_peptide 61..387

FT mat_peptide 61..387

FT wainble region against human IL-6 receptor

FT mat_peptide 61..387

FT mat_peptide 61..387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 bp RNA linear PAT 29-SEP-1997 mouse monoclonal antibody kappa type L chain
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                                                                                                                                                                                                                                                                                      301 GAAGACATTGCCACTTACTTTTTGCCAACAGGGTAACACGCTTCCGTACACGGTTCGGAGGG
  181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGGGTCCCATCA
                                                                                                                                                                                                                                                          GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACTTCGGAGGG
                                                                         GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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Pred. No. 7.2e-114;
Mismatches 0; Indels
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100.0%; Score 381; Di
Best Local Similarity 100.0%; Pred. No. 7.2.
Matches 381; Conservative 0; Mismatches
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/organism="Mus musculus"
/mol_type="genomic RNA"
/db_xref="taxon:10090"
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Mus musculus (house mouse)
Mus musculus
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MUSIVJR 393 bp mRNA linear ROD 25-MAY-1995
Mus musculus germline immunoglobulin light chain variable region
and joining region mRNA, 5' end.
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ASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQED
IATYFCQQGNTLPWTFGGGTKLEIKRADA"
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AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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Mus musculus
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 393)
Miller, D.J. and Rodriguez, M.

A monoclonal autoantibody that promotes central nervous system remyelination in a model of multiple sclerosis is a natural autoantibody encoded by germline immunoglobulin genes
J. Immunol. 154 (5), 2460-2469 (1995)
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Original source text: Mus musculus (strain SJL/J) hyperimmunized
spleen mRNA.
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germline; immunoglobulin light chain; joining region; variable
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//strain="sJL/J"
/strain="sJL/J"
/cell_line="SCH94.03"
/cell_type="hypridoma"
/lissue_type="hyperimmunized spleen"
/note="variable region and joining region; putative"
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/product="immunoglobulin light chain"
/protein id="AAA67439.1"
/db_xref="GI:829183"
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/function="leader peptide"
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/organism≃"Mus musculus"
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/product="unnamed"
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Matches 367; Conserv
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Modifyers, M. and Miller, D.J.
Monoclonal antibodies which promote central nervous system remyelination
Patent: US 5591629-A 1 07-JAN-1997;

Location/Qualifiers
1. 339
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                                          Length 381;
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                                        DB 10;
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Pred. No. 1.1e-106;
0; Mismatches 13;
                                        Score 359.2; DB 10
Pred. No. 1.1e-106;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 bp
Sequence 1 from patent US 5591629.
133380.1 GI:1824171
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96 c 89 g
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Best Local Similarity 96.6%;
Matches 367; Conservative (
                                          94.3%;
96.6%;
                                                                            Matches 367; Conservative
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product="Ig kappa chain"
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/product="Ig Appa chain"
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IATYPCQEGNTLPYTFGGGSKLEIKR"
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A to mRNA.
Location/Qualifiers
                                                                                                                                                 240
                             GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
                                                                                                                                                                                                           AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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Brigido, M. M. and Stollar, B. D.
Two induced anti-Z-DNA monoclonal antibodies use VH gene segments related to those of anti-DNA autoantibodies
J. Immunol. 146 (6), 2005-2009 (1991)
1900879
                                                GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCGGGAGACAGAGTCACC
                                                                                        ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                         121 ATCAGTTGCAGGCAAGTCAGGACATTAGCAATTATTAAACTGGTATCAGCAGAAACCA
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1 ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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M60019
M60019.1 GI:196423
C-region, J-region, immunoglobulin light cimmunoglobulin-kappa.
Mus musculus (house mouse)
Mus musculus
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12. .395
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/gene="IgM"
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Mus musculus Ig light chain leader and variable region Vk V gene family mRNA, partial cds.
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Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology
Program, Oklahoma Medical Research Foundation, 825 NE 13th Street,
Oklahoma City, OK 73104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 381)
White, K.D., Frank, M.B., Foundling, S. and Waxman, F.J.
Effect of immunoglobulin variable region structure on C3b and C4b
                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 GATGGAACTGTTAAACTCCTGATCTACACATCAATATTACACTCAGGAGTCCCAGCA
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Pred. No. 3.6e-106;
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96406984
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Mus musculus
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72. .356
/gene="lgM"
357. .395
/gene="lgM"
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/db_xref="G1:2806076"
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GQDISNYLNWYQQKPDGTVKLLVYYTSRLHSGVPSRVSGSGSGTDYSLTISNLEQEDI
ATYFCQQGNTLPYTFGGGTKLEIK"
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93.2%; Score 355.2; DB 10; Length 378;
Best Local Similarity 96.5%; Pred. No. 2.2e-105;
Matches 363; Conservative 0; Mismatches 13; Indels 0;
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Sequence 4 from patent US 5777085.
AR016717
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1. >378
/gene="IgK"
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343. .>378
/gene="IgK"
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58. .342
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                                                                                                                                 /translation="MMSSAQFLGLLLCFQGTRCDIOMTQTTSSLSASLGDRVTISCR
ASQDISNYLMWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQED
IATYFCQQGNTLPWTFGGGTKLBIK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
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                    /cell type="hybridoma (NS-1 x spleen cells) post DNP-BSA
immunīzations"
                                                                                                                                                                                                                                                                                    /note="encodes R1 through FR3 of immunoglobulin V-kappa"
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AF045496
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    .381
    /product="immunoglobulin light chain variable region"
/note="member of the murine Vk V gene family"

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                                                                /codon_start=1
/producie="immunoglobulin light chain precursor"
/protein_id="AAB42151.1"
/db_xref="GI:1041801"
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                                                                                                                                                                                                                                                                                                                                                                                     Length 381;
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Pred. No. 1.2e-105;
0; Mismatches 15; Indels
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92 c 83 g 101 t
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/note="leader region"
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      sex="female"
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96.1%;
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Matches 362;
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Mus musculus Balb/c anti-platelet integrin gplIb/IIIa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A humanized antibody specific for the platelet integrin gpIIb/IIIa
J. Immunol. 152 (6), 2968-2976 (1994)
94194058
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
Submitted (14-JAN-1994) Man Sung Co, Protein Design Labs., Inc., 2375 Garcia Ave, Mountain View, CA 94043, USA
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Co,M., Yano,S., Hsu,R.K., Landolfi,N.F., Vasquez,M., Cole,M.S.,
Tso,J.T., Bringman,T., Laird,W., Hudson,D., Kawamura,K. and
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0
                                                                                                                                                                                                                Length 381;
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                                                                   1 (bases 1 to 381)
Co.M.Sung. and Tso.J.Yun.
Humanized antibodies reactive with GPIIB/IIIA
Patent: US 5777085-A 4 07-JUL-1998;
Location/Qualifiers
                                                                                                                                                                                                             Score 351.2; DB 6;
Pred. No. 4.6e-104;
0; Mismatches 18;
                                                                                                                                                        /organism≃"unknown"
92 c 83 g
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  GI:3972994
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Best Local Similarity 95.3%;
Matches 362; Conservative
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U05217.1 GI:460600
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2 (bases 1 to 381)
                                          Unknown.
Unclassified.
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Suzuki,K.
                          Unknown
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/protein_id="AAA18224.1"
/db_xref="G1:460601"
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/fb_xref="G1:460601"
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/fb_yref="G1:460601"
/fb_y
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Mus musculus monoclonal antibody BBK-2 light chain mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGATGTCCTCTGCTCAGTTCCTTGTTTGCTTGTTTTTCAAGGTACCAGATGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 972)
Lee,U.H., Kwack,K., Park,J.W. and Kwon,B.S.
Direct Submission
Submitted (0.37AN-2002) Department of Biological Sciences, University of Ulsan, Ulsan 680-749, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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92 c 83 g
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                                                                                                                                        mol_type="mRNA"
strain="Balb/c"
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KTSTSPINVKFNRNEC"
263 c 204 g 231 t 3 others
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41._.745
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Location/Qualifiers
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ME4 Light Chain V MAb ME4 light chai Coding strand for DNA encoding mouse p146 k3. Syntheti CDNA encoding Sequence encoding

Sequence encoding
Human IL-1 chimeri
Murine immunoglobul
RM641 H.Chain vari
CDNA for humanised
Ganglioside-associ
CDNA for humanised
Activating polypep
Activating polypep
Activating polypep
Activating polypep
Murine consensus 1
Chimeric 4H6 antiChimeric 4H6 anti-

Title: Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Searched:

Database

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Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
plasmid; pPM-k3; pPM-h1; ss.
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                                                                                                                                                                                                                                                                                             AAA89072
AAA89088
AAA27323
AAC91015
AAC91016
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AAAS1004
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ABT14041
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AAV07641
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AAA89073
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W09219759-A1
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19-FEB-1992;
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30-MAR-1993
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287.2
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Anti-CD4 antibody
Mab SCH94.03 light
Mouse C4G1 Ig light
Variable region of
Mouse anti-human F
Mouse anti-human F
MAD VL17E6 light C
                                                                              October 24, 2003, 02:25:30 ; Search time 189.538 Seconds (without alignments) 5426.282 Million cell updates/sec
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| AIDSI/gcgdata/geneseq/geneseqn.embl/NA20018.DAT:*
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                                                                                                                                                         1 ATGGTGTCCTCAGCTCAGTT.......GGACCAAGCTGGAAATAAAT 381
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                                                                                                                                                                                                                                               5105512
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAQ36607
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AAQ45662
AAV36741
AAT59500
AAV34426
                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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359.2 359.2 351.2 351.2 351.2 349.6 348.6

Score

No No

Result

Murine anti-integr Bispecific CD3-L6F DNA encoding an im DNA encoding recom

Anti-human seminal DNA encoding immun

us-09-114-285a-28.rng

Bendig

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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD WT 15.1 is deposited as clone 15-1/p3/14 (ECACC alpha or beta anti-CD4 antibody is used with at least one anti-1L2R alpha or beta antibody. Individually the antibodies are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit transplant rejection at low doses without significantly reducing the general immune response. See also AAQ36608-Q36616. (Updated on 10-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synergistic antibody compsn. for use as immunosuppressant -comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%; Score 359.2; DB 14; Length 381; 96.6%; Pred. No. 5.8e-102; tive 0; Mismatches 13; Indels 0;
                                                                                                                  /*tag= b
/note= "J2 region begins at position 346"
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                                        Location/Qualifiers
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91DE-4143214.
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Matches 367; Conservative
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                                                                                                                                                                                                                                                                            The sequences given in AAQ30755-56 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PMI which (Updated the plasmids pPM-k3 and pPM-h1. (Updated on 25-MAR-2003 to correct PM field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGTGTCCTCAGGTCCTTGGTCCTTGTTGTTTCAAGGTACCAGATGT
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T-helper cell inhibition; transplant rejection; MAb;
interleukin-2 receptor; ss.
                                                                                                                                                          Reconstituted human antibody to human interleukin-6 receptor -
has low antigenicity and contains mouse V-region complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 381 BP; 106 A; 94 C; 84 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 381; DB 13; Best Local Similarity 100.0%; Pred. No. 9.1e-109; Matches 381; Conservative 0; Mismatches 0;
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                                                           Sato
                                                                                                                                                                                                                                      Disclosure; Page 121-122; 207pp; Japanese.
                                                         Saldanha JW,
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                                                               181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIIb; monoclonal antibody; platelet agglutination; humanised antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the mouse C4G1 immunoglobulin light chain. See AAQ45663 for the heavy-chain coding sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contg. immunoglobulin specific for the GP-IIB and -IIIA - for treating disorders related to vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
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/note= "C4G1 light chain"
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P-PSDB; AAR39265.
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09-JUN-1992;
11-SEP-1992;
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                                                                                                                                                                                                                                                  Monoclonal antibody, MAD; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases of
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                                      GGGACCAAGCTGGAAATAAA 380
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                                                                                                                                                                                                                                                                                                                                                                                                     181 GATGGAATTGTTAAACTCCTGATCTACTACATCAACATTACACTCAGGAGTCCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; antibody C4G1; light chain; humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation; ss.
                                                                                                                        1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                                                                                                                                                                                                                             ATCAGITGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
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                                       DB 14; Length 381;
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  T; 0 other;
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                                                                              18;
                                     92.2%; Score 351.2; DB 1.
larity 95.3%; Pred. No. 1.8e-99;
Conservative 0; Mismatches 18
BP; 104 A; 92 C; 83 G; 102
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91US-0812111.
92US-0895952.
92US-0944159.
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(YAMA ) YAMANOUCHI PHARM CO
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/product= '
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                                                          Local Similarity
les 362; Conserv
  Sequence 381
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09-JUN-1992;
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Matches
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                                                                                                                                                                                                                 This is the nucleotide sequence of the mouse antibody C4G1 light chain, used in the method of the invention involving the creation of a humanised immunoglobulin (1g) derived from the mouse C4G1 antibody. The humanised Ig is capable of binding to GPIID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute myocardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extracorporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPIID/IIIa on their surfaces, for the detection of GPIID/IIIa antigens or for isolating platelets. (Updated on 25-MAR-2003 to correct PA field.)
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New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.8e-99;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 381 BP; 104 A; 92 C; 83 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.2%; Score 351.2;
95.3%; Pred. No. 1.8
                                                                                                                                                       Disclosure; Fig 2A; 35pp; English
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Matches 362; Conservative
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is used for generating a mouse anti-human Fas ligand monoclonal antibody. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antiagonist can be a partial fas antiagon peptide containing the extracellular part of the protein, but lacking the signal sequence, an anti-Fas intibody, or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    failure, ischemic heart disease, acute kidney failure, graft-versus-host disease, ischemic restenosis of the heart, liver or kidney, and endotoxic shock, and also as an organ reservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AIGAIGICCICIGCTCAGTICCTIGGICTCCTGTTGCTCTGTTTTCAAGGIACCAGAIGT
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                                                                                                                                                                                                                                                                       Fas ligand; Fas antagonist; apoptosis related disease; liver disease;
                                                                                                                                                                                                                                                                                          heart failure, kidney failure; graft-versus-host disease; antibody; myocardial infarction; ischemic restenosis; endotoxic shock; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encodes the light chain of the mouse antibody F919-9-18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "F919-9-18 light chain"
/note= "the stop codon is not indicated"
                                                                                                                                                                                                                             Mouse antibody F919-9-18 light chain encoding cDNA.
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ilarity 95.0%; Pred. No. 5.7e-99;
Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       graft-versus-host disease or liver disease
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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  361 GGCACCAAGCTGGAAATCAA 380
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OSAKA BIOSCIENCE INST.
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                                                                                                        AAV34426 standard; cDNA; 381
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27-DEC-1996;
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nes 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-apoptosis inducing human Fas ligand, monoclonal antibody, F919. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis B/C, human immunodeficiency virus, graft/host disorders, ulcerative collitis or sequelae of myocardial infarction. The antibody may also be used to treat such diseases.
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graft versus host disease; ulcerative colitis; sequelae; myocardial infarction; mouse; murine; monoclonal; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes the light chain of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Vasquez M;
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95.0%; Pred. No. 5.7e
ive 0; Mismatches
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                                                                                                      Location/Qualifiers
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OSAKA BIOSCIENCE INST
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95JP-0188480.
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Matches 361, Conservative
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matrix interactions caused by alphaV integrin; which blocks tumo development and which has no cytotoxic activity, may be used to treat tumours, especially melanoma (but also glioma, carcinoma) optionally coupled to a cytokine such as interleukin-2. The monoclonal antibody may also be used for diagnostic imaging of tumours and assesment of tumour growth when conjugated to a radiolabel or a radio opaque-agent.
                                                                                                                                      Indels
                                                                                           Sequence 381 BP; 105 A; 88 C; 85 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody, chimera, light, heavy, chain, variable, antigen; diagnosis; cancer; tumour; ss.
                                                                                                                                      19;
                                                                                                               91.5%; Score 348.6; DB 1
ilarity 95.0%; Pred. No. 1.2e-98;
Conservative 0; Mismatches 19
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88US-0241744.
88US-0243739.
88US-0253002.
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(first entry)
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Matches 360; Conserv
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08-SEP-1988;
13-SEP-1988;
04-OCT-1988;
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04-MAR-1993
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                            GATATCCAGATGACACAGACTACATCCTCCTGTTTGCCTCTCTGGGAGACAGAGTCACC
                                                                          GATGGAACTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                                                                                                                                                          GGAGATATTGCCACTTTTTGCCAACAGGGTAGTACGCTTCCGTGGACGTTCGGTGGA
                                                                                                     GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                 AGGTTCAGTGGCAGTGGGACTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A monoclonal antibody which reacts only with the alphav chain of human alphav integrins; which blocks attachment of alphav integrin bearing cells to integrin substrate; which reverses established cell
                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody; MAb; integrin; cell-matrix interaction;
tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
imaging; detection; radiolabel; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Figure 17a; 54pp; English.
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61..381
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P-PSDB; AAR99003.
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Rosell E;
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DB 17; Length 381;
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121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone (AAT43440) codes for the light chain variable region the WAW06215) of mouse monoclonal antibody (Mab) ME4, and extends from the end of the Oligo-dC tail to the Vappa jucktion. It was obtd. from an ME4 hybridoma cDNA library by screening with a mouse C kappa region probe. MAD ME4 (IgG1) binds to an antigen that is expressed on the surface of human melanoma and lung, breast, colon and ovary carcinomas, but not on most normal adult tissues. Heavy chain and light chain variable region (see also AAT4334-43) sequences can be used with human constant region sequences to express mouse-human chimeric antibodies in transformed host cells. The antibodies have specificity to human tumour antigens and can be used for human cancer treatment and diagnosis.
                      Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
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/*tag= a
/product= Me4 light chain V region
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                                                                                                                                                            Location/Qualifiers
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88US-0240624.
88US-0241744.
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89US-036401.
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Best Local Similarity 94.7
Matches 360; Conservative
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19-JUN-1989;
21-JUL-1989;
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06-SEP-1988;
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                                                                                                                                                                                                                                                                                                                         Shown is the nucleotide sequence from the end of the oligo-dC tail to the Jkl-Ck junction. The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and avariable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAb) ME4. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                              Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour
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91.3%; Score 348; DB 11; Length 444;
Best Local Similarity 94.7%; Pred. No. 1.9e-98;
Matches 360; Conservative 0; Mismatches 20; Indels C
                                                                                                                    Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
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                                                                                                                                                                                                                                                                                      Claim 13; Page 123 + Fig 29; 173pp; English.
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                                                                                                                  Better MD, Horwitz AH, Robinson RR,
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89US-0367641
89US-0382768
                                                      (ITGE-) INT GENETIC ENG INC. (INGE-) INGENE INT GENETIC.
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(first entry)
                                                                                                                                                    WPI; 1990-115825/15.
                                                                                                                                                                          P-PSDB; AAR09426
19-JUN-1989;
21-JUL-1989;
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13-FEB-1997
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                                                                                                                                                                                                                                                                61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                      181 ATCAGTTGCAGGGCAAGTCAGGACATTACCACTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                           181 GATGGAACTATTAAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                                                                                                                                                                                                      121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                             1 ATGGTGTCCTCAGCTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse, human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis; tumour therapy; cytostatic; gene; ds; light chain variable region.
antibody-dependent cellular cytotoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                          ;
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                                                                                                                    Query Match
91.3%; Score 348; DB 20; Length 444;
Best Local Similarity 94.7%; Pred. No. 1.9e-98;
Matches 360; Conservative 0; Mismatches 20; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding mouse antibody light chain variable region #4
                                                                                       Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGGACCAAGCTGGAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 GGCACCAAACTGGAAATCAA 440
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94US-0364001.
88US-0240624.
88US-0243.
88US-0243.739.
88US-0253002.
89US-036761.
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27-DEC-1994;
06-SEP-1988;
08-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1988;
04-OCT-1988;
19-JUN-1989;
21-JUL-1989;
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     301 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCAGTGGAGCAA 360
                                                                                                                           GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                 GAAGATTTTGCCACTTACTTTTGCCAACAGGGTAATATACTTCCTCGGACGTTCGGTGGA 420
                                                          AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes the light chain variable region of murine antibody MB-. The sequence was used to create chimmeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodise also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody; treatment; human cancer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         аB
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/note= "partial CDS, no termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 strand for mouse ME4 light chain variable region.
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                                                                                                                                                                                                  GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                        GGCACCAAACTGGAAATCAA 440
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94US-0364001.
88US-02410624.
88US-0243739.
88US-025302.
99US-0382768.
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(first entry)
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P-PSDB; AAW85062.
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06-MAY-1991;
27-DEC-1994;
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16-APR-1999
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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen bound by the ING-1 antibody, where the ING-1 is produced by cell line (HB9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an immunoassay method for detecting an antigen in a sample by contacting a label detectable antigen in the sample with the antibody, detecting the label and relating the detected label to the presence of the antigen; cuse in an immain by contacting the antibody with a part of the animal suspected of containing the antigen; and for killing cells carrying an antigen by contacting the cells with the antibody and cletced label to the presence of the antibody with the antibody and allowing the killing to cocur. The antibodies are useful in tumour diagnosis and therapy. The chimeric antibodies bind to the surface of human tumour cells but do not bind detectably to normal cells, e.g., fibroblasts, endothehial cells or epithelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues implant the samilbodies may mediate selective destruction of imply that these antibodies may mediate selective destruction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determinants on the chimeric antibodies increases their resistance to rapid clearance from the body relative to the original murine mabs. This resistance to clearance enhances the potential utility of these chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies, as well as their derivatives, in tumour diagnosis and therapy. This sequence encodes a mouse antibody light chain variable region used in the creation of an anti-human tumour antigen-antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The presence of human rather than murine antigenic
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                                                                                                                                                                   Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-1 antibody
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                                                Chang CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 444 BP; 109 A; 122 C; 94 G; 119 T; 0 other;
                                                s,
                                                Lei
                                           Robinson RR,
                                                                                                                                                                                                                                                                       Example 3; Fig 29; 101pp; English.
(XOMA ) XOMA TECHNOLOGY LTD.
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                                                                                              2003-196707/19.
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                                                                                                                     P-PSDB; ABUS8896
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GGGACCAAGCTGGAAATAAA 380

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                                                                                                                                                                                         Human, antibody, interleukin-6, receptor; IL-6R, light chain, L; H; heavy chain, variable region, mouse, monoclonal; hybridoma; AUK146-15; plasmid; p146k3; p146-h1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTGTCCACACCTCAGTTCCTTGGTCTCTCTGGTGATCTGTTTTCAAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAQ30759 and AAQ31337 were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK146-15 which (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AIGGIGICCICAGCICCAGITCCITGGICTCCTGITGCICTGITITCAAGGIACCAGAIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.1%; Score 343.2; DB 13; Length 381; 93.9%; Pred. No. 5.7e-97; Indels 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reconstituted human antibody to human interleukin-6 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 381 BP; 106 A; 90 C; 86 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 127-128; 207pp; Japanese.
                                                                                                                                                                                                                                                                          Location/Qualifiers
1.60
/*tag= a
61.381
/*tag= b
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421 GGCACCAAACTGGAAATCAA 440
                                                                  B
                                                                  AAQ30759 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 93.9%;
Conservative
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                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-398882/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 357; Conserv
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                                                                                                                                                                                                                                                                                                                                                               WO9219759-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-1992;
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                                                                                                                        25-MAR-2003
30-MAR-1993
                                                                                                                                                                                                                                                                               Key
sig_peptide
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                                                                                              AAQ30759;
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                                        RESULT 13
                                                      AAQ30759
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to treat such diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
15-AUG-1991
                                                              Matches 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9107493-A
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                                         Query Match
                                                      Best Local
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           240
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                      181 GATGGAACTGTTAAACTCCTGATCTACGATACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                  241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCAGAGGAA 300
                                                                                                301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                301 GAAGATATTGCCAGTTACTTTTGCCAACAGGGTTATACGCCTCCGTGGACGTTCGGTGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the light chain variable region of the murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAb) KM1259. KM1259 is produced by the hybridoma FERM BP-5134, which was prepared by immunising Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAb can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
           GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                      AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody against alpha-chain of human interleukin 5 receptor -
useful for diagnosis and treatment of respiratory allergic diseases,
                                                                                                                                                                                                                                                                                                        Complementarity determining region; CDR; light chain; treatment; variable region; murine; mouse; human; interleukin 5; IL-5; receptor; alpha chain; monoclonal antibody; hybridoma; detection; assay; diagnosis; allergic respiratory disease; chronic bronchitis; da
                                                                                                                                                                                                                                                                                     cDNA encoding light chain variable region of KM1259 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koike M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Pages 122-123; 238pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                            GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                        Hanai N,
                                                                                                                                                                                                                       AAT73611 standard; cDNA; 382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK
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/*tag= a
61..381
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Takatsu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. chronic bronchitis
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Nakamura K,
                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
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           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GAAGATATTGCCACTTACTTTTGCCAACAGGGTTATACGCTTCCGTACACGGTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AGGITCAGIGGCAGCGGGTCIGGAACAGAITATICICICACCATIAGIGACCTGGAGCAA 300
                                                                                                                       09
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                                                                                                                                            1 ATGATGTCCTCTGCTCAGATCCTTGGTCTCCTGTTTTTCAAGATATCAGATGT
                                                                                                                                                                                                     61 GATATCCAGATGACACCAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                       121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                         GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG
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                                                                                                                                                                                                                                                                                                                    121 ATCGGTTGCGGGACAGTGAGGACATTATCAATTATTTAAACTGGTATCGGAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                  181 GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                                                                       1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                               Gaps
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                                       DB 18; Length 382;
                       Score 318.4; DB 18; Legal No. 1.8e-95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= mouse MAb 1C11 L(kappa)-chain
variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding light (kappa) chain variable region 1C11 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.
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Seguence 382 BP; 102 A; 89 C; 90 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibodies; immunoconjugates; HIV; AIDS;
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                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                       88.8%;
93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ12061 standard; DNA; 402
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(first entry)
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                                                          Similarity 93.2
54; Conservative
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(GREC ) GREEN CROSS CORP.
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P-PSDB; AAR12359

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 ATCACTIGCAGIGCAAGICAGGCCATIAGCAATTATTIAAACTGGIATCAGCAGAAACCA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 GATGGAACTGTTAAACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 AGGTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GAAGATATTGCCACTTACTATTGTCAGCAGTATAGTAAGCTTCCGTGGACGTTCGGTGGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGTGTCCTCAGCTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                            This sequence encodes the light (kappa) chain variable (V) region of a mouse monoclonal antibody (MAb), 1C11, specific for an HIV-1 viral antigen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 1C11 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme conjugates, in association with e.g. toxins for HIV treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                        to detect, kill and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.6%; Score 333.6; DB 12; Length 402; 92.4%; Pred. No. 5.7e-94; ive 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 402 BP; 108 A; 99 C; 88 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                They can also be used in diagnosis of HIV.
See also AAQ12056-60 and AAQ12056-63.
(Updated on 25-MAR-2003 to correct PA field.)
(Updated on 25-MAR-2003 to correct PI field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                      New chimeric mouse-human antibodies - used remove {\rm HIV}\textsc{-1} antigen from sample
                                                                                                     Disclosure; fig 13; 107pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.4
Matches 351; Conservative
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Search completed: October 24, 2003, 03:57:07 Job time : 191.538 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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BQ918407. 1459 bp mRNA linear EST 20-AUG-2002 AGENCOURT 8885602 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6397382 5', mRNA sequence. BQ918407 GI:22333105 EST.
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Detheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 1459)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: Capbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrapa by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LilaMai3895 row: c column: 15
High quality sequence start: 165
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                                                                   BY23531
BF581992
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AW406323
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                            RESULT 1
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 BQ918407 AGENCOURT
BI152061 602916512
BF123422 601760623
BI455041 603173343
                                                                                              October 24, 2003, 03:39:05 ; Search time 1673.61 Seconds (without alignments) 5532.953 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                           22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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BF123422
BI455041
                                                                     nucleic search, using sw model
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Listing first 45 su
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em_estfum::
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em_gss_mus: *
em_gss_pxo: *
em_gss_phg: *
em_gss_vr1: *
gb_gss1: *
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seq length: 200000000
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88.9
88.4
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Score

No. Result

339.4 338.6 336.8 327.2

BF580940 602100636
BF57803 602094455
BF57803 60209448
BF518192 602094448
AZ313441 M0016K06
BG956348 602831226
CB958057 AGENCOURT
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BQ881840 AGENCOURT
BQ881840 AGENCOURT
CB987506 AGENCOURT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus-
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                               1 ATGGTGTCCTCAGCTCCAGTTCCTTGGTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGT
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0
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89.1%; Score 339.4; DB 13;
Best Local Similarity 93.2%; Pred. No. 7.2e-94;
Matches 355; Conservative 0; Mismatches 26; I
ity sequence stop: (
Location/Qualifiers
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BF123422 669 bp mRNA linear EST 24-OCT-2000 601760623F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4023749 5',
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Stem cell origin."
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Library constructed by Life Technologies. Investigator
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NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.
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http://image.llnl.gov
Plate: LLAM11180 row: h column: 04
High quality sequence stop: 827.
Location/Qualifiers
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/organism="Mus musculus"
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                                                                                                                                                                                                    /mol_type="mRNA"
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AUTHORS
TITLE
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602889345FI NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5044690 5', mRNA sequence.
BI103114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 ATCAATTGCAGGGCAAGTCAGGACATTACCAATTATTTAAATTGGTATCAGCAGAAACCA 185
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                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMIGS row: e column: 12
High quality sequence stop: 820.
Location/Qualifiers
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                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="tumor, gross tissue"
/dev stage="7" months"
/lab_host="DHIOB"
/clone lib="NHIOB"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
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Nus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
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                            cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9282 row: n column: 06
High quality sequence stop: 649.
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                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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/clone="IMAGE:4023749"
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/strain="C57BL/6J"
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Best Local Similarity 94.1%;
Matches 350; Conservative
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                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1122 row: i column: 11

High quality sequence stop: 706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db.race="raxxon:10090"
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Average insert size 1.75 kb. Constructed by Life
Technologies Note: this is a NCI_CGAP Library. |"
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                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
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                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/strain="FVB/N"
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                                    Mus musculus (house mouse)
   GI:14554007
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                                                    Mus musculus
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Matches 344; Conserv
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                                                    ORGANISM
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BF580940
LOCUS
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                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9813 row: g column: 09
High quality sequence stop: 694.
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224032 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA</u>
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81.9%; Score 312; DB 10;
Best Local Similarity 90.5%; Pred. No. 1.6e-85;
Matches 344; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
78 a 153 c 137 g 158 t
                                                                                                                                                         BF582283 626 bp mRNA linear EST 12-DEC-2000 602101109F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224267 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 626)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9814 row: a column: 04
High quality sequence stop: 624.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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370 CACCAAGGTGGAAGTCA 386
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                                                       BF578083 966 bp mRNA linear EST 12-DEC-2000 C0209479E1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4209015 5',
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/lab host==INAGE:4209015"
/lab host==DH10B (T1 phage-resistant)"
/clone lb="NOT GGAP_CO24"
/note="Organ colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NOI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9774 row: e column: 16
High quality sequence stop: 614.
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92.3%; Pred. No. 8.9e-85;
ive 0; Mismatches 27; Indels
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/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
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Matches 348; Conservative
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                                                                                                                                                                                                                                                                                                                                                BY235531 BIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930042F10 5', mRNA sequence.
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UKL.http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Kawai,J., Konno,H., Miyazaki,A.
T.: Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
264 CTCTCACCATTAGCAACCTGGAGCAAGAAGATA-TGCCACTTACTTTTGCCAACAGGGTA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                        323 AAGCGCTTCCTCGGACGTTCGGTGGAGGCACCAAGGTGGAAATCAA 368
                                                                                                         335 ACACGCTTCCGTACACGTTCGGAGGGGGGGCCAAGCTGGAAATAAA
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/note="Organ: mammary; Vector: pcNV-SPORT6; Site 1: Sal1; Site_2: NOtI; Cloned unidirectionally.
Site_2: NotI; Cloned unidirectionally.
Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 774)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM9282 row: e column: 23
High quality sequence stop: 736.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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78.8%; Score 300.4; DB 10; Length 774;
Best Local Similarity 93.6%; Pred. No. 6.6e-82;
Matches 324; Conservative 0; Mismatches 21; Indels 1;
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:4023550"
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mamalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 772)

NIH-MGC http://mgc.nci.nih.gov/,

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.
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/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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Pred. No. 1.4e-80;
0; Mismatches 19
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/strain="C57BL/6J"
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="TMAGE:4219618"
/lab host="DH10B (T1 phage-resistant)"
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/clone="TMAGE:4219618"
/clone="TMAGE:4219618"
/note="Organ: Colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 ATTACACATCAAGTTTACACTCCAGGAGTCCCATCAAGGTTCAGTGGCAGTGGGTCTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTCCTGTTGCTCTGTTTTCAAGGTACCAGATGTGATATCCAGATGACACAGACTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGCAGTTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTATTAAACTCCTGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 TIGCCAATTATTTAAACTGGTATCAGCAGAAACCAGATGGAACTGTTAAACTCCTGATCT
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Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CLNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov. o column: 11 High quality sequence stop: 715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 AACAGGGTAACACGCTTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 294.8; DB 10;
Pred. No. 3.6e-80;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 89.3%;
Matches 317; Conservative
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316 GAAGATTTTGCAGACTATTACTGTCTACAACGTGATGCGTATCCGTGGACGTTCGGTGGC 375
                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                        BG963548.1 GI:14351185
                                                                                                                                      mRNA sequence.
402 CTCCCAC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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Best Local 9
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                                                                                                               DEFINITION
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ORIGIN
                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
COMMENT
                                                      RESULT 13
BG963548
LOCUS
                                                                                                                                                        ACCESSION
                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM22 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAAGGTACCAGATGTGATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                 SIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 GGTATCAGCAGAAACCAGATGGAACTGTTAAACTCCTGATCTATTACACATCAGGATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 TGGGAGACAGAGTCACCATCAGTTGCAGGGCAAGTGAGGACATTAGCACTTATTTAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 TCAGCAACCTGGAACCTGAAGATATTGCCACTTACTATTGTCAGCAGTATAGTTAAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.8%; Score 262.2; DB 2090.9%; Pred. No. 4.6e-70; iive 0; Mismatches 28
                                                                                                                                                                                            Std Error: 0.00
                                                                                                                                                                                          Insert Length: 10000 Std Error:
Plate: 0016 row: K column: 06
Seg primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                        High quality sequence stop: 730.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0016K06"
                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 279; Conservative
plasmid inserts
Unpublished
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Best Local Similarity
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ORIGIN
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BG963548 112-JUN-2001
602831226F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4985791 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db zref="taxon:10090"
/clone="IMAGE:4985791"
/lab host="bHIOB (II phage-resistant)"
/clone lib="WCI CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 178 c 167 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AGGITCAGIGGCAGIGGGICIGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AGGITCAGIGGCAGIGGGICIGGGICAGAITAITCICICACCAICAGCAGCCIAGAGICT 315
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 714)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ATCAGGGCTCCTGCTCAGTTTCTTGGCATCTTGTTGCTGTCTTCCAGGTGCTCCAGATGT
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                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0994 row. c column: 08
High quality sequence stop: 712.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/lab host="DH10B" (phage-resistant)"
/clone lib="NIH MGC_113"
/clone lib="NIH MGC_113"
/note="Corgan: spleen; Vector: pOTB7; Site_1: Xho1; Site_2: Drote="Corgan: spleen; Vector: pOTB7; Site_1: Scori, Scori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ881840 888 bp mRNA linear EST 16-AUG-2002 AGENCOURT 8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:62957255', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2502 row: g column: 22
High quality sequence stop: 655.
High quality sequence stop: 655.
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                                                                                                                                                                                                                                                                                                                                                                       GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                               241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 888)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:6295725"
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/clone="Dright: Pooled-clandular; Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc);
Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thypid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCGACATATGGCT-3' and 3' adaptor sequence: 5'-CACGGCCGACATATGGCT-3' and 3' adaptor sequence: 5'-CACGGCCGACATATGGCT-3' and 3' adaptor sequence: 5'-CACGGCCGGCGCGCACATATGGT-0T(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3:5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM148 row: g column: 15
High quality sequence stop: 558.
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AGENCOURT 13785358 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30351230 5′, mRNA sequence.
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Search completed: October 24, 2003, 05:48:28 Job time : 1680.61 secs

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SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
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ADDRESSEE:
STREET: 30
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1 ATGGTGTCCTCAGCTCAGTT......GGACCAAGCTGGAAATAAAT 381
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE: 158
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MEANING SON STATE: D.C. COUNTRY: USA ZIP: 20007-5109

COMPUTER READABLE FORM: READABLE FORM: REDIUM TYPE: Floppy disk COMPUTER READABLE FORM: COMPUTER: IBM PC COMPATIBLE OFFICE OFFICE SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: DO-DEC-1993

CLASSIFICATION NUMBER: US/08/137,117D

FILING DATE: 24-APR-1992

PRIOR APPLICATION DATA: APPR-1992

PRIOR APPLICATION NUMBER: UP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA: APPR-1991

APPLICATION NUMBER: UP 3-95476

FILING DATE: 25-APR-1991

APPLICATION NUMBER: 25,258

REGISTRATION NUMBER: 25,258
                              US-08-040-224-9
PCT-US95-05262-3
US-08-040-224-13
US-08-040-204-15
US-08-040-204-15
US-08-040-204-14
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US-08-040-204-12
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US-09-813-659-29
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US-08-436-717-28
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iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08436717;
Patent No. 5817790
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB1-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT: INFORMATION:
NAME: WEGONER, HAIOLI CREGISTRATION NUMBER: 25.258
REGISTRATION NUMBER: 25.258
REGISTRATION NUMBER: 25.258
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACCAAGCTGGAAATAAAT 381
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Patent No. 5591629
GENERAL INPORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: MONOCLONAL A
                                                                                                                                                                                                                                                                                                                                                                                       (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 381 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 381; Conservative
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1..381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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180 240

120

9

360

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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GAAGATATTGCCACTTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 300
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    CENTRAL NERVOUS SYSTEM REMYELINATION
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINAT NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSE: ABMILLON, Brook, Smithy & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                              COMPUTER FLADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
FLING DATE: 29-APR-1994
ATTONENY/AGENT INPORMATION:
NAME: GRANAHAIN:
REFERENCE/DOCKET NUMBER: 27,227
RESPERENCE/DOCKET NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAY92-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-861-6340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 393 Date pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 96.6
Matches 367; Conservative
                                                                                                                CITY: Lexington
STATE: Massachusetts
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LOCATION:
                                                                                                                                                             COUNTRY:
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; Sequence 1, Application PC/TUS9505262 ; GENERAL INFORMATION:

PCT-US95-05262-1

RESULT 4

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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCCCTCTCTGGGAGACAGAGTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Argaricricricatriccristriccristricristricristricaaggraccagargr 60
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APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Lexington
CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PE: Floppy disk
COMPUTER: PRE-FILE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 359.2; DB 5;
Pred. No. 4e-105;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER:
FILING DATE: April 29, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Particia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV92-01 PCT
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
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96.6%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.6'
Matches 367; Conservative
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                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY:
; LOCATION:
PCT-US95-05262-1
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301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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APPLICANT: PIULATS, Jaume
APPLICANT: ROSELL, Elisabet
APPLICANT: ADAN, Jaume
APPLICANT: ADAN, Jaume
APPLICANT: HAHN, Diane
APPLICANT: HAHN, Diane
TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,699A
FILING DATE: US/08/574,699A
FILING DATE: DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: 33,302
REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: MERCK 1743
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Millen, White, Zelano & Branigan, P.C. STREET: 2200 Clarendon Blvd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide
LOCATION: 1..60
OCHER INFORMATION: /function= "Leader sequence"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..381
                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08574699A
; Patent No. 5985278
; GENERAL INFORMATION:
                                                                                                                          361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                               361 GGCACCAAGCTGGAAATCAA 380
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..381
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HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
CLONE: 72-17E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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NAME/KEY:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AGGTTCAGTGGCAGTGGGACTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATCAGTTGCAGGCCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GATGGAATTGTTAAACTCCTGATCTACTACACATCAACATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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                                                                           Sequence 4, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE: 03-MAY-1993
PFILING DATE: 03-MAY-1993
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
APPLICATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 30,223
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 351.2; DB 1;
Pred. No. 1.4e-102;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.3%;
Matches 362; Conservative
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; LOCATION:
US-08-458-516-4
                                                              US-08-458-516-4
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AGGITCAGIGGCAGIGGGICTGGAACAGAITAITCTCTCACCATTAACAACCTGGAGCAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.9%; Score 346.4; DB 1; Length 381; 94.5%; Pred. No. 4.8e-101; ive 0; Mismatches 21; Indels 0
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS: 158
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: 70169 & Lardner STREET: 3000 K Street; N.W., Suite 500
CITY: Weahington STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: EAP Compatible
COMPUTER: EAP Compatible
COMPUTER: EAP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 300
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: WP 4-32084
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 9-5476
FILING DATE: 25-APR-1991
ATTORNEY ABENT IN-PROMATION: NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY ABENT IN-PROMATION: NAME: WEGNET HATORICALION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPAK: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 904136
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.5
Matches 359; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-137-117D-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGAACTGTTAAACTCCTGATCTTCTACACATCAAAATTACACTCAGGAGTCCCATCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 348.6; DB 2; Length
Pred. No. 9.5e-102;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 208.728
OTHER INFORMATION: /function= "CDR-2 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 325.751
OTHER INFORMATION: /function= "CDR-3 sequence"
                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 130..162
OTHER INFORMATION: /function= "CDR-1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

LOCATION: 352..381

CTHER INFORMATION: /function= "FR-4 sequence"

MS-08-574-699A-1
                                NAME/KEY: misc feature
LOCATION: 61..129
OTHER INFORMATION: /function= "FR-1 sequence"
                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
IOCATION: 163..207
OTHER INFORMATION: /function= "FR-2 sequence"
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: 229.324
OTHER INFORMATION: /function= "FR-3 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACCAAGCTGGAAATAA 379
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 360; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-137-117D-36
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-836-561-28
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                   GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: JONES, Seeven
APPLICANT: JONES, Seeven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILING DATE:

CLASSIFICATION NOMBER: US/US/150/71

RIGHS APPLICATION DATA:

APPLICATION NUMBER: US/08/137,117

FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544

FILING DATE: 24-APR-1992

APPLICATION NUMBER: UP 4-32084

FILING DATE: 19-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 3-95476

FILING DATE: 25-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: WEGLERATION NUMBER: 25.258

REGISTRATION NUMBER: 25.258

REGISTRATION NUMBER: 25.258

TELEPHONE: (202) 672-5300

TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                   STREET: JOOR & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  361 GCCACCAAGTTGGAAATCAA 380
                                                                                                                                                                                   Sequence 36, Application US/08436717 Patent No. 5817790
                                                                 361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..381
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NAME/KEY:

LOCATION:

US-08-436-717-36
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                                                                                                                                                                     US-08-436-717-36
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TELEX: 9
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90.9%; Score 346.4; DB 1; Length 381;

Query Match

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180
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                              Gaps
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APPLICANT: FURUYA, AKIKO
APPLICANT: INDA, AKINIAO
APPLICANT: IDDA, AKINIAO
APPLICANT: ANAZAWA, Hideharu
APPLICANT: HANAI, No. 6018032uo
APPLICANT: HANAI, No. 6018032uo
APPLICANT: HANAI, No. 6018032uo
APPLICANT: HANAIN MILIDODA AGAINST HUMAN INTERIBURIAN RECEPTOR AIPHA CHAIN
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                              Indels
                                                                                       1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGCTCTGTT
Best Local Similarity 94.5%; Pred. No. 4.8e-101;
Matches 359; Conservative 0; Mismatches 21;
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REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMINICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION UNDER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 6018032
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APPLICANT: KOIKE, Masamichi
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PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 354; Conserv
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US-08-408-133-5
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FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. 6538111uo
TAKATSU Kiyoshi
TITLE OF INVÉNTION: Antibody Against Human Interleukin-5
                                                                                                                                                                      Length 382;
                                                                                                                                                                       Score 338.4; DB 3; Length
Pred. No. 1.7e-98;
0; Mismatches 26; Indels
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COMPUTER: IBM Compatible
COMPATER: BM Compatible
COMPATE: SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
RENT APPLICATION DATA:
FILING DATE: 05-NO. 6538111-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
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Patent No. 6538111
GENERAL INFORMATION:
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                                 28:
                                                                                                                                                                       88.8%;
93.2%;
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2
SEGUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                          MOLECULE TYPE: CDNA
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US-09-434-122-28
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Best Local
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Patent No. 5750078
GENERAL INFORMATION:
APPLICANT: SHITMEA, Kenya
APPLICANT: HANAI, No. 5750078uo
APPLICANT: MIYAI, Mimoru
APPLICANT: MIYAI, Hiromasa
APPLICANT: KUWANA, Yoshihisa
TITLE OF INVENTION: Process for Producing Humanized Chimera
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 338.4; DB 4;
Pred. No. 1.7e-98;
0; Mismatches 26;
                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Lawrence, III. Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-434-122-28
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                                                                                                                                                                                                                            TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 382 base pairs
                                                                                                                                                                                                                                                      TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.8%;
                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: singl
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325 GAAGATATTGCCACTTACTTTTGTCATCAGTATAGTAAGCTTCCGTGGACGTTCGGTGGA 384
                                                                                                                                                                                                 Sequence 5, Application US/08454683
Patent No. 5807548
GENERAL INFORMATION:
APPLICANT: SHITARA, Kenya
APPLICANT: HARAI, No. 5807548uo
APPLICANT: MIYAJI, Hiromasa
APPLICANT: MIYAJI, Hiromasa
APPLICANT: MIYAJI, Hiromasa
TITLE OF INVENTION: Process for Producing Humanized Chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon & Vanderhye, P.C. STREET: No. 5807548th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/408,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US 08/292,178
FILING DATE:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEPT-1992
ATTORNEY/AGENT INFORMATION:
                                            361 GGGACCAAGCTGGAAATAAA 380
                                                                                        385 GCCACCAAGCTGGAAATCAA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLOWAGE CRAMFORD, Arthur R
TELECOMMUNICATION INFORMATION:
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
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OTHER INFORMATION:
FEATURE:
NAME/KEY: Sig_peptide
LOCATION: 25..84
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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LOCATION: 85..408

US-08-454-683-5
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: KM-641
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                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
                                                                                                                                                                                                      US/08/408,133
                                                                                                                                                                                                                                                                                                                                      US 07/947,674
                                                                                                                                                SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408.17:
                       COUNTRY: U_S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-SEPT-1992
ATORNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-400
TELEFAX: (803)816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.6%;
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: N
ORIGINAL SOURCE:
STRAIN: KM-641
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Best Local Similarity 90.5
Matches 344; Conservative
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LOCATION: 25...84
OTHER INFORMATION:
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; LOCATION: 85..408
; OTHER INFORMATION:
US-08-408-133-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 25..408
OTHER INFORMATION:
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Patent No. 643709B
APPLICANT: SHITMRA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, WAMORU
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/225,322B
CURRENT PILING DATE: 1999-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 322.4; DB 2;
Pred. No. 2.2e-93;
0; Mismatches 36;
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INPORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663 .
REFERENCE/DOCKET NUMBER: 249-74
TELECOMUNICATION INFORMATION:
TELEFRAM: 7038164100
INFORMATION FOR SEQ ID NO: 5:
SEGUENCE CHARACTERISTICS:
LENGTH: 408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TODOLOGY: linear
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Best Local Similarity 90.5%;
Matches 344; Conservative
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85..408
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25..84
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LOCATION:
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LOCATION:
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; LOCATION:
US-08-454-680-5
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US-09-225-322B-9
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GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA

APPLICANT: HAMAI, NOBUO

APPLICANT: HASEGAWA MAMORU

APPLICANT: HASEGAWA MAMORU

APPLICANT: MIXAI, HIROMSA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA

TITLE OF INVENTION: ANTIBODY

NUMBER OF SEQUENCES:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: ARLINGTON

STATE: VA

COUNTY: USA
    Query Match

84.6%; Score 322.4; DB 1; Length 408;
Best Local Similarity 90.5%; Pred. No. 2.2e-93;
Matches 344; Conservative 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,680
FILING DATE: 31-MAY-1995
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/408,133
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/292,178
FILING DATE: 17-ANG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION NUMBER: US 07/947,674
FILING DATE: 17-SEP-1992
PRIOR APPLICATION NUMBER: UP 3-238375
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US-08-454-680-5
'Sequence 5, Application US/08454680
'Patent No. 5866692
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Length 408; Indels

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Patent No. 649566
GENERAL INFORMATION:
APPLICANT: SHITARA, KERYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGARA, MAWORU
APPLICANT: MYSAJI, HIROMASA
APPLICANT: MYSAJI, HIROMASA
APPLICANT: MYSAJI, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REPREBNCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
NAME/KEY: CDS
LOCATION: (25)..(408)
NAME/KEY: mat peptide
LOCATION: (85)..(408)
NAME/KEY: sig peptide
LOCATION: (25)..(84)
US-09-225-122B-9
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Pred. No. 2.2e-93;
0; Mismatches 36;
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR PILING DATE: 1992-09-18
PRIOR PILING DATE: 1991-09-18
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NOS: 19
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90.5%;
                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.5
Matches 344; Conservative
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US-09-764-304-9
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61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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Pred. No. 2.2e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 36; Indels
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: US 07/947,674
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 24, 2003, 05:50:34 Job time: 58.8788 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.5<sup>3</sup>
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (25)..(408)
NAME/KEY: mat_peptide
LOCATION: (85)..(408)
NAME/KEY: sig_peptide
LOCATION: (25)..(84)
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RESULT 1
US-08-779-784-20
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Sequence 1, Appli
Sequence 1, Appli
Sequence 28, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
GENERAL INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, App
Sequence 97, Appl
Sequence 70, Appl
                                                                                                                                                                                                 October 24, 2003, 03:57:16; Search time 904.875 Seconds (without alignments) 1129.179 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGTGTCCTCAGCTCAGTT......GGACCAAGCTGGAAATAAAT 38:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-268-883-4

US-10-288-384-9

US-10-283-349-28

US-09-764-304-9

US-10-265-713-9

US-10-265-713-9

US-10-265-713-9

US-10-283-349-102

US-10-283-349-97

US-10-283-349-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1792395 segs, 1340900451 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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381
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                             Copyright
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Match
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Maximum DB s
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                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
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Sequence 347, App
Sequence 2, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 3, Appli
Sequence 28, Appli
Sequence 13, Appli
Sequence 11, Appli
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Sequence 5, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 125, Appli
                                                                                                                                                                                                                                                 Sequence 1210, Ap
Sequence 1210, Ap
Sequence 1, Appli
Sequence 27, Appl
    Appl
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           Sequence 72, R
Sequence 6, R
Sequence 29, R
    Sequence 33,
12 US-10-310-674A-33
9 US-09-905-243-72
10 US-09-813-659-65
14 US-10-141-908-6
10 US-09-813-659-34
10 US-09-480-28-2
14 US-10-191-908-30
14 US-10-141-908-3
14 US-10-141-908-3
14 US-10-141-908-3
15 US-09-861-294-1
16 US-09-861-294-1
17 US-09-861-294-1
18 US-10-367-506-1
18 US-09-924-099-27
18 US-10-367-804-5
18 US-10-367-804-5
18 US-10-367-804-5
18 US-10-367-804-3
18 US-10-368-883-10
2 US-10-368-883-10
3 US-10-268-883-10
3 US-10-268-883-10
3 US-10-367-804-3
10 US-09-859-053-29
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276
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## ALIGNMENTS

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Sequence 20, Application US/08779784

Publication No. US20020164325A1

GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Maller, David J.
APPLICANT: Makura, Kunihiko
ITILE OF INVENTION: REMYELINATION OF CENTRAL NERVOUS SYSTEM
ITILE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: Floor
CITY: Hackensack
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esg., David A.
REGISTRATHON NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 87, Sequence 22, A Sequence 3, A Sequence 91,

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Publication No. US20030138862A1
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HIA-DR Antibodies and the Methods of Using Thereof
FILE REPRENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/80 60/329,178
PRIOR PLING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
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                                                                                                                                                            Score 359.2; DB 12; Length 393; Pred. No. 1.4e-110; 0; Mismatches 13; Indels 0;
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                        FastSEQ for Windows Version 4.0
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                              Query Match 94.3%;
Best Local Similarity 96.6%;
Matches 367; Conservative
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Best Local Similarity 95.3
Matches 362; Conservative
                                                                                                      ; ORGANISM: Mus musculus
US-10-010-729-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mouse US-10-268-883-4
                                                                 393
                      SOFTWARE: Fa
SEQ ID NO 63
LENGTH: 393
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                                                                                    TYPE: DNA
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Sequence 63, Application US/10010729

Publication No. US20030185827A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Miller, David J.

APPLICANT: Roderiguez, Moses

APPLICANT: Passe, Larry R.

ITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous TITLE OF INVENTION: ASystem

ITLE OF INVENTION: ASystem

ITLE OF INVENTION: ASystem

ITLE OF INVENTION: ASystem

CURRENT APPLICATION NUMBER: US/10/010,729

CURRENT FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 09/320,787

PRIOR PILING DATE: 1999-05-28

PRIOR PILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-06-28

PRIOR FILING DATE: 1999-06-08-08

PRIOR PLING DATE: 1994-04-29

NUMBER OF SEQ ID NOS: 80
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                                                                                                                                                                                                                                                                                     Length 393;
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Pred. No. 1.4e-110;
0; Mismatches 13; Indels
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TELEPAX: 201-487-5800
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.6%;
Matches 367; Conservative
                                                                                                                                                                                                                             1..393
                                                                                                                                                                                                                           ; LOCATION:
US-08-779-784-20
                                                                                                                                                                                                     NAME/KEY:
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US-10-010-729-63
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                                                                                                                                                                                                                                                                                NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-0ct-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-283-349-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: ISM Compatible
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                         Sequence 28, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
                                                          361 ĠĠĊŔĊĊŔŔĠĊŢĠĠŔŔŖĊŔŔ 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 28
                                                                                                                                                                                                                                                                    FURUYA, Akiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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Best Local Similarity
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                                                                          ATCAGTTGCAGGTCAAGTCAGGACATTAGCAAATATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                  240
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GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 120
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Pred. No. 2.3e-107;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAGATA, Shigekazu
APPLICANT: YATOMI, Takehiro
APPLICANT: YOMI, Takehiro
APPLICANT: SUDA, Takashiro
TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
FILE REFERENCE: 1110-0307P
CURRENT APPLICATION NUMBER: US/10/084,139
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                         GGGACCAAGCTGGAAATAAA 380
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Publication No. US20030109416A1
GENERAL INFORMATION:
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)..(381)
US-10-084-139-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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US-10-084-139-1
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Best Local S
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205 GATGGAACTGTTAAACTCCTTTTTACTCATCAAATTTACACTCGGGAGTCCCATCA 264
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HANGEAN, MENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAMA, MANORU
APPLICANT: HASEGAMA, MANORU
APPLICANT: HASEGAMA, MANORU
APPLICANT: MIXAJI, HIROMASA
APPLICANT: MIXAJI, HIROMASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-10.1
CURRENT APPLICATION NUMBER: US/09/225,32B
PRIOR FILING DATE: 1999-01-05
PRIOR FILING DATE: 1999-01-05
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-17
PRIOR FILING DATE: 1995-09-17
PRIOR FILING DATE: 1995-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATCHILIN VET: 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                   265 AGGTTCAGTGGCGGTGGGTCCGGGACAGATTATTCTCTCACCATCAGCAACCTGGAGCCT
                                                  121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
                                                                                           145 ATCAGTTGCAGTGCAAGTCAGGACATTAGTAATTTTAAACTGGTATCAACAGAAACCA
                                                                                                                                                                                                                                                                                                                                GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG
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                                                                                                                                           181 GATGGAACTATTAAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA
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OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
FEATURE:
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Pred. No. 3.5e-98;
0; Mismatches 36; ]
                                                                                                                                                                                                                                                                                                                                                                                                                            361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACCAAGCTGGAAATCAA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10166626 Publication No. US20030166876A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 90.55
Matches 344; Conservative
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LOCATION: (25)..(84)
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LOCATION: (25)..(408)
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181 GATGGAACTGTTGAACTCCTGATCTACCACATCAAGATTACAGTCAGGAGTCCCATCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09764304

Sequence 9, Application US/09764304

Sequence 9, Application US/09764304

Sequence 9, Application US/0906036A1

GENERAL INFORMATION:
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
CURRIT ENTERNION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304

CURRENT APPLICATION NUMBER: US/09/25,322

EARLIER PILING DATE: 1099-01-05

EARLIER FILING DATE: 1999-01-05

EARLIER FILING DATE: 1999-03-21

EARLIER PILING DATE: 1999-03-21

EARLIER PILING DATE: 1999-03-21

EARLIER PILING DATE: 1994-08-17

EARLIER FILING DATE: 1994-08-17

EARLIER FILING DATE: 1994-08-17

EARLIER FILING DATE: 1994-08-17

EARLIER FILING DATE: 1991-09-18

NUMBER: OF SEQ ID NOST: 19

SOFTWARE: PATCATION NUMBER: USO/947,674

EARLIER FILING DATE: 1991-09-18

NUMBER: OF SEQ ID NOST: 19
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Pred. No. 3.5e-98;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                     361 GGGACCAAGTTGGAAATAAA 380
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OTHER INFORMATION: cDNA KM-641
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Best Local Similarity 90.5%;
Matches 344; Conservative
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LOCATION: (85)..(408)
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121 ATCAGTTGCAGGCCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
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                                                                                                                                    25 Argargrecrerecreagricerregienecrererrerrerreaggiage
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84.2%; Score 320.8; DB 14; Length 408;
Best Local Similarity 90.3%; Pred. No. 1.2e-97;
Matches 343; Conservative 0; Mismatches 37; Indels 0;
      DB 14; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CLUSTONE
STATE: COUNTRY: U.S.A.

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Tam PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/195,752
FILING DATE: 16-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                Indels
    84.6%; Score 322.4; DB 14; 90.5%; Pred. No. 3.5e-98; ive 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HANAI, NOBUO
KUMAAN, YOSHIHISA
HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRIOR AFFILCATION DAIM:
APPLICATION NUMBER: US/09/393,385B
FILING DAIE: 27-UUM-96
TELECOMMUNICATION INFORMATION:
                                                                                          1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTG
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SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-195-752-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-195-752-19
GENERAL INFORMATION:
HPPLICANT: NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
HITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELEPHONE: (703)816-4000
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                                                Conservative
                         Best Local Similarity
Matches 344; Conserv
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      Query Match
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                                                                                               GATATCCAGATGACACAGACTGCATCCTCCCTGCCTCTCTGGGAGACAGAGTCACC 144
                                                                                                                                                         121 ATCAGTIGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                   GATGGAACTATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
                                                                                                                                                                                                                                                                                                                                             AGGITCAGIGGCAGIGGGICIGGAACAGAITATICICICACCAITAACAACCIGGAGCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                              GATGGAACTGTTAAACTCCTGATCTTTTACTCATCAAATTTACACTCGGGAGTCCCATCA 264
                                                                                                                                                                                                                                                                                                                                                                                      265 AGGTTCAGTGGCGGTGGGTCCGGGACAGATTATTCTCTCACCATCAGCAACCTGGAGCCT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATATTGCCACTTACTTTTGTCATCAGTATAGTAAGCTTCCGTGGACGTTCGGTGGA 384
ATGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTTTTTCAAGGTACCAGATGT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HASEGÁMA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE KEFEKENEL 347-LUJ

CURRENT PILING DATE: 2002-10-08

PRIOR APPLICATION NUMBER: US/09/225,332

PRIOR APPLICATION NUMBER: US/09/225,332

PRIOR PILING DATE: 1999-01-05

PRIOR PILING DATE: 1999-01-05

PRIOR PILING DATE: 1995-05-31

PRIOR PILING DATE: 1995-05-31

PRIOR PILING DATE: 1995-03-21

PRIOR PILING DATE: 1994-08-17

PRIOR PILING DATE: 1994-08-17

PRIOR PILING DATE: 1994-08-17

PRIOR PILING DATE: 1992-09-17

PRIOR PILING DATE: 1992-09-17

PRIOR PILING DATE: 1992-09-17

PRIOR PILING DATE: 1992-09-17

PRIOR PILING DATE: 1991-09-18

PRIOR PILING DATE: 1991-09-18

SOFTWARE: PATENTIN VUMBER: JP 3-238375

PRIOR PILING DATE: 1991-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 GCCACCAAGCTGGAAATCAA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10265713
Publication No. US20030095964A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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; LOCATION: (25)..(84)
US-10-265-713-9
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NAME/KEY: CDS
LOCATION: (25)..(408)
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                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                     Score 309.6; DB 1.
Pred. No. 6.9e-94;
); Mismatches 44
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CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
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                 SEQUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 102
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88.4%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                          Similarity
                                                                                                                                                              US-10-283-349-102
                                                                                                                                                                                                                              Best Local Sim:
Matches 336;
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                                      84
                       25 AIGATGTCCTCTGCTCAGTTCCTTGGTCTCCTGTTGTTTTCAAGGTACCAGATGT
                                                                                                                                                              121 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA
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FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskete
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 102, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 GCACCAAGCTGGAAATCAA 404
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COMPUTER READABLE FORM:
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DB 14;
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87.1%; Pred. No. 3.4e-91;
tive 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                             CURRENT TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION ATA:
APPLICATION DATA:
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/836,561
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: Pennie & Edmonds LLP
STREDT: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACCAAGGTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: singl
                                                                                                             COMPUTER READABLE FORM:
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Best Local Similarity 87.1
Matches 331; Conservative
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US-10-283-349-91
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FURUYA, AKIKO
NAKAWURA, KAZUYASU
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 304.8; DB 14; Length
Pred. No. 2.9e-92;
0; Mismatches 47; Indels
                                                                                                                                 NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
                                                                      APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
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                                                          FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                       LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 97:
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Best Local Similarity 87.6
Matches 333; Conservative
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US-10-283-349-70
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US.10-283-349-87
US.10-283-349-87
Sequence 87, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
HOUSE AREA ARIXO
NARAMURA, Razuyasu
IIDA, ARINICO
ANAZAWA, Hideharu
HANAI, No. US20030096977Aluo
HANAI, No. US20030096977Aluo
TITLE OF INVENTION Antibody Against Human Interleukin-5
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.7%; Score 300; DB 14;
86.8%; Pred. No. 1.2e-90;
ive 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGTGTCCTCAGCTCAGTTCCTTGGTCTCCTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSASLEDO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/836,561
FILING DATE: 09 *MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                       361 GGGACCAAGCTGGAAATAAA 380
                                                                                                                                                                                            361 GGGACCAAGGTGGAAATAAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
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LENGTH: 382 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 87
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Matches 330; Conserv
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Query Match
79.2%; Score 301.6; DB J
Best Local Similarity 87.1%; Pred. No. 3.4e-91,
Matches 331; Conservative 0; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY:
APPLICATION NUMBER: US/08/836,561
APPLICATION NUMBER: US/08/836,561
APPLICATION NUMBER: JP 232384/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFRAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 382 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
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COMPUTER READABLE FORM:
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                                                               61 GATATCCAGATGACACAGTCTCCATCCTCCTGTCTGCCTCTGTAGGAGACAGAGTCACC 120
                                                                                                        ATCAGTTGCAGGCAAGTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCA 180
                                                                                                                                                                                                                                                                                    AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAACAACCTGGAGCAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER KEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-04A-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-04G-1996
PRIOR APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: New Jersey
COUNTRY: USA
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US-08-779-784-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GAAGACATTGCCACTTACTTTTGCCAACAGGGTAACACGCTTCCGTACACGTTCGGAGGG 360
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                                                                                                                                                  1 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
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                                                              Gaps
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  Length 324;
                                                           Indels
  Score 299.2; DB 8;
Pred. No. 2e-90;
0; Mismatches 13;
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Query Match
Best Local Similarity 95.9%;
Matches 307; Conservative
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Search completed: October 24, 2003, 06:22:16 Job time : 908.375 secs

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Variable region of MAb VL17E6 light c p146 k3 procein pr Mouse MAb 1C11 L c Light (kappa) chai Human/murine IL-1

C4G1 Ig ligh

Rat immunoglobulin pKM641 LA2 immunog KM641 H chain vari Light chain variab CD19:zeta chimeric

Ganglioside GD3 sp Modified gangliosi

Murine immunoglobu

Ganglioside GD3 sp anti-CD22 monoclon

Ganglioside-associ Ganglioside-associ Murine consensus 1

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Human, antibody, interleukin-6; receptor; IL-6R; light chain; L;
heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
plasmid; pPM-k3; pPM-h1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21..127
/note= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Signal peptide"
                                                                                                                                                                     AAW21844
ABB82300
ABJ18571
                                                                                                                                                                                                                          AAY94216
AAB81999
AAW66098
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AAB49242
AAB81995
AAU75368
AAU75369
AAU75374
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AAU75373
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AAR30768
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ABG72265
AAU75365
AAU75370
AAR39265
AAW49809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR28670 standard; Protein; 127 AA
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(first entry)
pPM-k3 protein product.
93.6
993.6
991.7
990.3
989.3
886.8
86.8
86.8
86.7
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30-MAR-1993
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19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9219759-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1992
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 pPM-K3 protein pro
MAD SCH94.03 light
Anti-CD4 antibody
Mouse anti-thuman F
Mouse antibody F91
ME4 Light Chain V
MAD ME4 light chai
Mouse ME4 light chai
Mouse antibody light
                                                                                       October 22, 2003, 22:03:25; Search time 57.2462 Seconds (without alignments) 352.133 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                              A Geneseq 19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41981.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41985.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41985.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41980.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41980.DAT:*
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| SIDS1/gcgdata/geneseqfy-embl/AA41980.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41991.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/AA41999.DAT:*
| SIDS1/gcgdata/geneseqfy-embl/A
                                                                                                                                                                     MVSSAQFLGLLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
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                                                                                                                                                                                                                                                                 1107863
             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR28670
AAR84553
AAR32121
AAW11815
AAW60033
AAW062126
AAW85062
                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĮΩ
                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                           US-09-114-285A-29
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127
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128
128
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Match
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Post-processing:

Database

Minimum DB Maximum DB

Scoring table:

Searched:

Perfect score:

Sequence:

protein

6

Run ĕ

Canglioside GD3 sp Chimeric 4H6 anti-Ganglioside GD3 sp Diphtheria toxin/U Diphtheria toxin/U

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Score

Š. Result

638 621 621 621 621 621 621

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1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                        Hybridoma ATCC CRL 11627 was obtd. from a SJL/J mouse injected with spinal cord homogenate from a mammal uninfected with any demyelinating disease. The hybridoma produced a monoclonal antibody (SCH94.03) useful in promoting CNS remyelination. The SCH94.03 light chain amino acid sequence is given in AAR84553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppression; tissue transplantation; graft; L chain; V region; T-helper cell inhibition; transplant rejection; MAb; interleukin-2 receptor.
                                                                                                                                                                           Monoclonal antibodies which stimulate central nervous system re-myelination - are produced by hybridoma ATCC CRL 11627, for treating multiple sclerosis, and viral or post-neural diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 638; DB 16; Length 131;
Pred. No. 7.8e-42;
5; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-CD4 antibody MT 15.1 light chain variable region.
                                                                                                                                                                                                                                                             Disclosure; Page 36-37; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR32121 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal
21.115
/label= Variable
116.127
/label= J2
                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%;
 95WO-US05262.
                              94US-0236520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 121; Conservative
                                                                                               Rodriguez M;
                                                               (MAYO-) MAYO FOUNDATION
                                                                                                                               WPI; 1995-393077/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          131 AA;
                                                                                                                                              N-PSDB; AAT05311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTKLEI
   27-APR-1995;
                               29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE4143214-A1
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10-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1993
                                                                                               Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR32121;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                               the CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                         The sequences given in AAR28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody which comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous syste CNS; demyelination; multiple sclerosis; neural disease; therapeutic
                                                                                                              Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 661; DB 13; Length 127; 100.0%; Pred. No. 1.3e-43; ive 0; Mismatches 0; Indels 0
                                 Tsuchiya M;
                                 Saldanha JW, Sato K,
                                                                                                                                                                              Disclosure; Page 121-122; 207pp; Japanese.
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//label= Joining_region
129..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129..131
/label= C-kappa_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..20
/label= Leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR84553 standard; Protein; 131 AA.
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/label= CDR1
70..76
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109..117
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
1es 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAb SCH94.03 light chain.
(CHUS ) CHUGAI SEIYAKU
                               Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTKLEIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GTKLEIN 127
                                                              WPI; 1992-398882/48.
N-PSDB; AAQ30755.
                                                                                                                                                                                                                                                                                                                                           127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9530004-A1
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
Matches 127,
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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Peptide Mus sp.

Region Region Region Region Region

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Gaps

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us-09-114-285a-29.rag

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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MMSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas ligand, Fas antagonist, apoptosis related disease, liver disease, heart failure, kidney failure, graft-versus-host disease, antibody, myocardial infarction, ischemic restenosis, endotoxic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody reactive with Fas ligand capable of inducing apoptosis - used for diagnostic assay of Fas ligand in body fluids and for treatment of diseases in which Fas ligand/Fas antigen is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the light chain of the mouse anti-apoptosis inducing human Fas ligand, monoclonal antibody, 1919. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis LG, human immunodeficiency virus, garkf(host disorders, ulcerative colitis or sequelae of myocardial infarction. The antibody may also be used to treat such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 621; DB 18; Length 127; 93.7%; Pred. No. 1.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse antibody F919-9-18 light chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shirakawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 10; 164pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagata S,
/label= CDR_2
109..117
/label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                     (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                96US-0649100.
95JP-0188480.
                                                                                                                                                                                                                                      96WO-JP01820.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-108917/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsusue T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT59500.
                                                                                                                                                                                                                                                                                                   17-MAY-1996;
30-JUN-1995;
                                                                                                                         WO9702290-A1
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                                                                                                                                                                                23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Region
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                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the light chain variable region of a preferred anti-CD4 monoclonal antibody for use in the claimed synergistic composition. MAD MT 15.1 is deposited as clone 15-1/P3/14 (ECACC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R alpha or beta antibody. Individually the antibodiss are strongly inhibiting and when used together their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low see also AAQ36608-Q36616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                Synergistic antibody compsn. for use as immunosuppressant - comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-IL2R beta antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Fas ligand, antigen, neutral; antibody; apoptosis; HIV, induction, assay; enzyme linked immunosorbant assay; diagnosis; disease; hepatitis B; hepatitis C; human immunodeficiency virus; graft versus host disease; ulcerative colitis; sequelae; myocardial infarction; mouse; murine; monoclonal; treatment; complementarity determining region; CDR.
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0
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Pred. No. 5.3e-41;
6; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse anti-human Fas ligand antibody F919 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                              Scheuer W, Weidle U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
44..54
/label= CDR_1
70..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW11815 standard; Protein; 127 AA
                                                                                                                                                 (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 9; 18pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 94.9%; al Similarity 93.7%; 118; Conservative
      91DE-4143214.
                                                            91DE-4124759.
91DE-4143214.
                                                                                                                                                                                                           Kaluza B, Riethmueller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                 WPI; 1993-037582/05.
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                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ36607.
                                                            25-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Best Local
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AAW11815

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DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is used in the prodn. of a chimeric antibody mol. comprising two light chains and two heavy chains, each having a constant region (human) and a variable region (murine) having specificity to an antigen bound by murine monoclonal antibody (MAb) ME4. The chimeric antibodies can be used for any purpose for which the original murine MAbs can be used, with the advantage that they are more compatible with the human body. They are esp. used for the diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric mouse-human antibodies - prepd. using genes coding for constant human region murine variable region, esp. to 3 tumour
                                              Monoclonal antibody, chimera, light, heavy, chain, constant, variable, antigen, diagnosis, cancer, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 621; DB 11;
Pred. No. 1.5e-40;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 123 + Fig 29; 173pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAD ME4 light chain variable region.
ME4 Light Chain V Region (mouse)
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88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-115825/15.
N-PSDB; AAQ08608.
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Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA;
                                                                                                                                Mus musculus
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19-JUN-1989;
21-JUL-1989;
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13-FEB-1997
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  DE STANDAR SE STANDAR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is used for generating a mouse anti-humanes anti-budy. The invention provides the use of Fas antagonist as an agent for the treatment and prevention of apoptosis-related diseases. The Fas antagonist can be a partial Fas antigen peptide containing the search anti-fas antial Fas antigen peptide containing the search anti-fas anti-fas antibody. Or an anti-Fas ligand antibody, where the antibody is preferably a humanised antibody. The Fas antagonist is used in the treatment and prevention of diseases such as myocardial infarction, heart disease, ischemic restrements of the heart, liver or kidney, and endocoxic shock, and also as an organ preservative in transplantation. The agent is of low toxicity but effectively inhibits the Fas/Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents the light chain of the mouse antibody F919-9-18. This
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  "complementarity determining region (CDR)
                                                 "complementarity determining region (CDR)
                                                                                                  /note= "complementarity determining region (CDR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of Fas antagonist for treatment and prevention of apoptosis-related diseases - such as heart or kidney failure, graft-versus-host disease or liver disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 621; DB 19;
Pred. No. 1.5e-40;
7; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 86pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                   (MOCH ) MOCHIDA PHARM CO LTD. (OSAB-) OSAKA BIOSCIENCE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yatomi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9%;
                                                                                                                                                                                                                                                                                                                                         96JP-0290459.
96JP-0351718.
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(first entry)
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Best Local Similarity 93.7
Matches 118; Conservative
  'note=
                                                   /note=
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N-PSDB; AAV34426.
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                                                                                                                                                        WO9818487-A1
                                                                                                                                                                                                                                                                31-OCT-1997;
                                                                                                                                                                                                                                                                                                                 26-SEP-1997;
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04-MAR-1993
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Length 128; Indels

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Light chain variable region; murine antibody ME4; antibody ING-1; chimeric immunoglobulin; human tumour antigen; chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric antibody specific for human tumour antigen - useful as
                                                                                                                                                                                                                                                                                                                                                                                                               immunoassay, imaging or antitumour agent
                       Mouse ME4 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 29; 92pp; English.
 16-APR-1999 (first entry)
                                                                      treatment; human cancer
                                                                                                                                                                                                                                                                                                                                         Better MD, Chang CP,
                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-044574/04.
N-PSDB; AAV71158.
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                                                                                                                                                                     06-JUN-1995;
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27-DEC-1994;
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19-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
           Chimeric antibody; monoclonal antibody; ME4; antibody engineering; tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma; ovary carcinoma; melanoma; cancer; diagnosis; therapy; light chain.
                                                                                                                                                                                                                                                                                                                                                    Chimeric mouse-human antibodies - recognise a human tumour antigen, used for the treatment and diagnosis of human cancers
                                                                                                                                                                                                                                                                                                                                                                                                           The light chain variable region (AAW06215) of mouse monoclonal antibody ME4 is the product of a cDNA clone (AAT43440) isolated from a ME4 hybridoma cDNA library. MAb ME4 (IgG1) binds to an antigen that is expressed on the surface of human lung, breast, colon and ovary carcinomas and melanomas, but not on most normal adult tissues. The light chain and heavy chain variable regions (see also AAW06216) of ME4 can be linked to human constant regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and expressed in transformed host cells. Novel mouse-human chineric antibodies (see also AAW06209-14 and AAW06217-18) can be produced that have specificity to human tumour antigens for use in the treatment and diagnosis of human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.9%; Score 621; DB 18; Length 128; 93.7%; Pred. No. 1.5e-40; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                         Robinson RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                 88US-0240624.
88US-0241744.
88US-0243739.
88US-0253002.
89US-0367641.
89US-0364001.
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Best Local Similarity 93.77
Matches 118; Conservative
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N-PSDB; AAT43440.
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                                                                                                                                                                  06-SEP-1988;
08-SEP-1988;
13-SEP-1988;
                                                                                                                                27-DEC-1994;
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27-DEC-1994;
                                                                                 US5576184-A.
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19-JUN-1989;
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AAW85062
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Robinson RR;

Horwitz AH, Lei S,

9103-0659401. 9403-0364001. 8803-0240624. 8803-0241744. 8803-0243739. 8803-0253002. 8903-03827681.

95US-0466034 89WO-US03852

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
The present sequence represents the light chain variable region of murine antibody ME4. The sequence was used to create chimeric mouse-human immunoglobulins which recognise the human tumour antigen bound by antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The chimeric antibodies also have an antigen-binding site that competitively inhibits the binding of antibody ING-1, and mediate complement-dependent cytolysis of target cells or antibody-dependent cellular cytocoxicity to target cells. The chimeric antibodies can be used for therapeutic purposes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 621; DB 20;
Pred. No. 1.5e-40;
5; Mismatches 3;
                                                                                                                                                                                                                                                                            treatment of human cancer. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU58896 standard; Protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.7%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                    128 AA;
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(updated)

20-MAR-2003

AAW85062;

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The invention describes an antibody comprising a human constant region and a variable region having specificity for the human tumour antigen. Coming a deposited with ATCC, and the ING-1 is produced by call line HB9812 as deposited with ATCC, and the ING-1 is produced by call line the HB9812 as deposited with ATCC, and the antibody has the same affinity as the ING-1 for the human tumour antigen. The antibody is useful in an imaging method for revealing the presence of the antigen; for use in an imaging method for revealing the presence of a label-detectable containing the antigen, the presence of a label-detectable antigen in an antigen in an imaging method for revealing the presence of a label-detectable containing the antigen, detecting the label and relating the guspected of containing the antigen, detecting the label and relating the cattying an antigen by contacting the calls with the antibody and callowing the killing to occur. The antibodies are useful in tumour cells but do not bind detectably to normal cells, org., fibroblasts, endothelial cells or pepthelial cells in the major organs. The high biological activity of the chimeric antibodies against human tumour cell lines combined with minimal reactivity with normal tissues imply that these antibodies may mediate selective destruction of caping clearance from the body relative to the original murine mabs. This creases the colearance chameric antibodies increases their resistance to clearance enhances the potential utility of these chimeric antibodies, and contibodies, and continued an enumour cell as their derivatives, in tumour diagnosis and therapy. This is the amino acid sequence of a mouse antibody light chain arrival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody for detecting antigen in animal or killing cells carrying antigen comprises human constant region and variable region having specificity for human tumor antigen bound by ING-i antibody
                                                                                                                                                                                                                Mouse; human tumour antigen; anti-human tumour antigen-antibody; ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis; tumour therapy; cytostatic; light châin variable region.
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                                                                                                                                            Mouse antibody light chain variable region #4.
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94US-0364001.
88US-0240624.
88US-0241744.
88US-0253002.
89US-0357641.
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                                                                       (first entry)
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                                                                    16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6461824-B1
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06-SEP-1989;
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ABU58896;
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                                                                                                  61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDFATYFCQQGNILPRTFGG 120
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                                                       DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG
                                           1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                        Gaps
                                                                                                                                                                                                                                                                                                              Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIIb;
monoclonal antibody; platelet agglutination; humanised antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the sequence of the mouse C4G1 immunoglobulin light chain. See AAR39266 for the heavy chain sequence. The antibody is specific for the GPIIa/IIIb protein and inhibits platelet agglutination. The Ig is thus useful in the treatment of thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. contg. immunoglobulin specific for the GP-IIB and -IIIA protein - for treating disorders related to vascular thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                   l= complementarity_determining_region_1
   Length 128;
                      Indels
Score 621; DB 24;
Pred. No. 1.5e-40;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                       //label= signal_peptide
22..127
//label= light_chain
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2A; 54pp; Japanese.
                                                                                                                                                                                                               AAR39265 standard; Protein; 127 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR_2
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/label= CDR_3
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92US-0895952.
92US-0944159.
 93.9%;
93.7%;
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                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                      Mouse C4G1 Ig light-chain.
 Query Match
Best Local Similarity 93.7
Matches 118; Conservative
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-227275/28.
N-PSDB; AAQ45662.
                                                                                                                                  121 GTKLEI 126
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29-NOV-1993
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11-SEP-1992;
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/label= Framework
        Disclosure; Fig 2A; 35pp; English
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                                                                                                                                                               93.6%;
92.9%;
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/label= CDR1
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/label= CDR2
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                                                                                                                                                                                                                                                                                                                                                                  10-JAN-1997 (first entry)
                                                                                                                                                              Query Match 93.6
Best Local Similarity 92.9
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .127
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/label=
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                                                                                                                                               127 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
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                                                                                  1 MMSSAQFLGFLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKP
                                                                                                                                                                                                                                                                           Mouse, antibody C4G1, light chain; humanised; immunoglobulin; Ig; inhibition; antigen; cardiovascular disease; thromboembolic disorder; cancer; acute myocardial infarction; unstable angina; stroke; transient ischemic episode; pulmonary embolism; deep vein thrombosis; extracorporeal cardiopulmonary circulation.
                                                                  1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanised immunoglobulin which binds GPIIb/IIIa - derived from mouse C4G1 antibody, used for inhibiting platelet aggregation for treating cardiovascular and thromboembolic disorders.
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0
                                  Length 127;
                                                                                                                                                                                                                                                                                                                                                                                      /note= "complemetarity determining region"
70..76
                                                                                                                                                                                                                                                                                                                                                                                                            'note= "complemetarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "complemetarity determining region"
                                                 Indels
                                                                                                                                                                                                                                                            Variable region of mouse antibody C4G1 light chain.
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С
                                Score 619; DB 14;
Pred. No. 2.2e-40;
6; Mismatches 3;
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                           'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                 AAW49809 standard; Protein; 127 AA.
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                                 93.6%;
92.9%;
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92US-0895952.
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                                                                                                                                                                                                                                   (updated)
(first entry)
                                        al Similarity 92.9
117; Conservative
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                                                                                                                                       126
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                 127 AA;
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                                                                                                                                       GTKLEI
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09-JUN-1992;
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24-SEP-1998
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                                                                                                                     61
                                                                                                    61
                 Sequence
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                                                                                                                                                                                                                  AAW49809
                                 Query Match
Best Local
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Protein
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61 DGIVKLLIYYTSTLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGG 120
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                      chain, used in the method of the invention involving the creation of a humanised in the method of the invention involving the creation of a humanised ig is capable of binding to GPID/IIIa and inhibiting platelet aggregation and also the releasing reaction of platelets. The Ig can be used for treating cardiovascular diseases and thromboembolic disorders, e.g. acute mycoardial infarction, unstable angina, stroke, transient ischemic episodes, deep vein thrombosis and pulmonary embolism, extraocrporeal cardiopulmonary circulation. The Ig can also be used in diagnosing the presence and location of a thrombus, or certain types of cancer cells which develop GPID/IIIa on their surfaces, for the detection of GPIID/IIIa antigens or for isolating platelets.

(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody, MAb; integrin; cell-matrix interaction; tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2; imaging; detection; radiolabel.
This is the amino acid sequence of the mouse antibody C4G1 light
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 619; DB 19;
Pred. No. 2.2e-40;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21..43
/label= Framework region 1
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/label= Framework region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR99003 standard; Protein; 127 AA.
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Tsuchiya M;

Sato K,

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The sequences given in AAR29010-11 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody which comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                          90.6%; Score 599; DB 13; Length 127; 90.5%; Pred. No. 7.5e-39;
                                                                                                                                                                                                                    Disclosure; Page 127-128; 207pp; Japanese.
                                                                                                   Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR12237 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse MAb 1C11 L chain V region.
          92WO-JP00544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90WO-US06627.
                                 91JP-0095476
92JP-0032084
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(first entry)
                                                                         (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                     Matches 114; Conservative
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(GREC ) GREEN CROSS CORP.
(ZOMA-) ZOMA CORP.
                                                                                                   Jones ST,
                                                                                                                           WPI; 1992-398882/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTKLEI 126
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                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                   127 AA;
                                                                                                                                        N-PSDB; AAQ30759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1; chimera
          24-APR-1992;
                                 25-APR-1991;
19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1990;
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19-AUG-1991
                                                                                                   Bendig MM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
plasmid; p146-k3; p146-h1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVSSAQFLGLLLCFQVTRCDIQMTQTTSSLSASLGDRVIISCRASQDISNYLSWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                  A monoclonal antibody which reacts only with the alphav chain of human alphav integrins; which blocks attachment of alphav integrin bearing cells to integrin substrate; which reverses established cell matrix interactions caused by alphav integrin; which blocks tumour development and which has no cytotoxic activity, may be used to treat tumours, especially melanoma (but also glioma, carcinoma) optionally coupled to a cytokine such as interleukin-2. The monoclonal antibody may also be used for diagnostic imaging of tumours and assesment of tumour growth when conjugated to a radio opaque-agent.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                       New human integrin V chain-specific monoclonal antibody - and related DNA and hybridomas, for treatment and diagnostic imaging
                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                         91.7%; Score 606; DB 17; Length 127; 90.5%; Pred. No. 2.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                             Mitjans F, Piulats J;
                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Signal peptide"
21..127
/note= "Mature peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR29010 standard; Protein; 127 AA.
                                                                                                                                                                                           Claim 8; Figure 17a; 54pp; English
                                                             Hahn D,
         94EP-0120165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                   (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.5
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p146-k3 protein product
                                                                                                                                                                    tumours, esp melanoma.
                                                                                                 WPI; 1996-302345/31.
N-PSDB; AAT35050.
                                                             Goodman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTKVEM 126
                                                                                                                                                                                                                                                                                                                                                                127 AA;
         20-DEC-1994;
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                                                                         Rosell E;
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Gaps

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Indels

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8; Mismatches

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Gaps

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Score 590; DB 12; Length 127; Pred. No. 3.7e-38; 7; Mismatches 6; Indels

89.3%;

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DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DGTVKLLIYYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPWTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                  1 MMSSAÓFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKP 60
                       monoclonal antibody (MAb), 1C11, and is specific for an HIV-1
viral antigen. It is used in the construction of a chimeric
MAb comprising heavy and light chains having murine V regions
and human C regions. The chimeric MAbs are more effective than
murine MAb IC11 since they have an increased compatibility in
humans. The heavy and light chain V-regions are joined by
manipulating their respective joining (J) regions, to generate
c restriction enzyme recognition sites. The chimeric MAbs can be
used a immunoconjugates, in association with e.g. toxins for HIV
treatment. They can also be used in diagnosis of HIV.
C Greated on 25-MAR-2003 to correct PA field.)
(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                      1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
This is the light (kappa) - chain variable (V) region of a mous
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Best Local Similarity 89.7
Matches 113; Conservative
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                                                                                                                                                                The mouse VL gene product may be used to produce chimeric mouse-
human Abs against HIV-1 comprising human Ig constant regions and
murine variable regions. These novel sequence are useful in
treatment, diagnosis and prophylaxis of HIV infections, and may be
produced by a bacterial, yeast or mammalian expression system.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                     chimeric mouse human antibodies - used in treatment, diagnosis prophylaxis of HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light (kappa) chain variable region of murine 1C11 immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric mouse-human antibodies - used to detect, kill and remove HIV-1 antigen from sample
                                                                                                                                                                                                                                                                                                                     89.3%; Score 590; DB 12; Length 126; 89.7%; Pred. No. 3.7e-38; ive 7; Mismatches 6; Indels (
                 Robinson RR
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               Ghoshdasti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Better MD, Horwitz AH, Ghoshdasti P,
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                                                                                                                                      Disclosure; Fig 13; 108pp; English
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(GREC ) GREEN CROSS CORP.
               Better MD, Horwitz AH,
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                                            WPI; 1991-178106/24
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GenCore version (c) 1993 - 2003
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34	473	71.6	108	Н	KVMS73	kappa chain	
35	467	70.7	111	~	G38740	kappa chain	ы
36	465	70.3	129	7	D32513	kappa chain	pre
37	457	69.1	129	7	S52789	kappa chain	ы
38	453	68.5	123	(7)	S40331		ď
39	451	68.2	130	Н	KVMSM4	kappa chain	pre .
40	449	67.9	127	N	S40367	kappa chain	V-J
41	447	67.6	129	~	S40369		r.
42	445	67.3	129	~	540317		ď
43	443	67.0	129	7	S52793		ы
44	442	6.99	132	7	S40334	kappa chain	ч
45	439	66.4	125	7	S40349	chain	V-J
					ALIGNMENTS	ro.	
RESULT 1							
A34904							
Ig kappa chain	chain	precure	sor V re	gio	precursor V region (5-27) - mouse	ıse	
C;Species: Mus musculus (house mouse)	s: Mus	musculı	snoy) sr	ë =			
	27-Jul-	1990 #6	sednence	re	vision 27-Jul-1990	-1990 #text_change 21-Jan-2000	
C; C;Accession: A34904	ion: A3	4904					
R;	W.D.;	Herron	, ט.ט, ר	BG	mundson, A.B.;	, Voss Jr., E.W.	
J. Biol.	Chem.	265, 13	Biol. Chem. 265, 133-138, 1990	199			
A.Title: Active site	Active	site f	structum	e a	A, Title: Active site structure and antigen bin b. Reference number: 234903: MITD:90094387: PMT	binding properties of idiotypically PMID:2104617	lly cross
	ion: A3	4904					
A;Status	: preli	minary	; not co	адшо	red with conce	A; Status: preliminary; not compared with conceptual translation	
A; Molecule type: mRNA	le type	: mRNA		1			

A;Molecule type: mkNA A;Residues: 1-126 <BED> C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-109/Domain: immunoglobulin homology <IMM>

s-read

61 2 VSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPD Gaps ., Length 126; 0; Indels 95.6%; Score 632; DB 2; 93.7%; Pred. No. 2.3e-48; live 8; Mismatches 0 Query Match 95.6%; Best Local Similarity 93.7%; Matches 118; Conservative ò

GTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGG 121 GTVKLLIYYTSKLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGG 120 122 TKLEIN 127 62 61 g ò g ò

121 TKLEIN 126 В Interest of the precursor V region (W-T151) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000
C;Accession: PH1224
R;Weissenhorn, W ; Scheuer, W.; Kaluza, B ; Schwirzke, M.; Reiter, C:; Flieger, D.; Lenz A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and on A;Reference number: PH1224
M;Neterson: PH1224
A;Accession: PH1224
A;Molecule type: mRNA
A;Residues: 1-127 <WEI>A;Accession: PH224
A;Molecule type: mRNA
A;Accession: M

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R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea A;Reference number: JL0076; MUID:89096973; PMID:3211160
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                                                                                                                                                                                                                                                                                                                             LIYYTSRLHSGVPSRFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI
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                                                                                                                                                                                                    7 FLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKL
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A;Residues: 1-115 <KAA>
A;Residues: 1-115 <KAA>
A;Residues: 1-115 <KAA>
A;Cross-references: GB:M2793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A;Note: the authors translated the codon AGG for residue 30 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Kcywords: immunoglobulin
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                                                                Score 607; DB 2; Length 122;
Pred. No. 3.4e-46;
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Pred. No. 3.3e-44;
4; Mismatches 0; Indels
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Pred. No. 9e-44;
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Fi.7-2-96/Domain: immunoglobulin homology <IMM>Fi.20-40/Region: complementarity-determining 1
Fi.56-62/Region: complementarity-determining 2
                                                                                                                                   6; Mismatches
   F;30-104/Domain: immunoglobulin homology <IMM>
                                                                91.8%;
95.0%;
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97.38;
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Best Local Similarity 96.5%;
Matches 111; Conservative
                                                                                                                                   Matches 114; Conservative
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C; Accession: A56406
R; Sanz, I: Capra, J.D.
Proc. Natl. Acad. Sci. U.S. A. 84, 1085-1089, 1987
A; Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination genera
A; Reference number: A26406
A; Molecule type: DNA
A; Residues: 1-128 cSAN>
A; Residues: 1-128 cSAN>
A; Cross-references GB:M15519
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: A29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. (Chem. 262, 13579-13583, 1987
A;Fitle: Nucleotide and translated amino acid sequences of cDNA coding for the varial A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Reference number: A28612; MUID:88007582; PMID:3115981
A;Residues: 1-122 cCHE>
A;Residues: 1-122 cCHE>
A;Cross-references: GB:M1160; GB:J02815; NID:9196895; PIDN:AAA38824.1; PID:9196896
A;Note: the authors translated the codon TTC for residue 1 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Spate: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000;
Accession: A26406
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F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig light chain V region #status predicted <WAT>
F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                       Length 127;
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Pred. No. 9.7e-48;
                                                                                                                                Score 627; DB 2;
Pred. No. 6.4e-48;
6; Mismatches 2;
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                                                                                                                                94.9%;
llarity 93.7%;
Conservative
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Best Local Similarity 93.7%;
Matches 118; Conservative
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Matches 118; Conserv
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Gaps

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapi hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar C;Superfamily: immunoglobulin V region; immunoglobulin homology
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R;Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A;Title: Complete amino acid sequence of light chain variable regions derived from five A;Reference number: A01927; MUID:82150934; PMID:6801658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-108 <SIE.
A;Eserimental source: strain A/J
A;Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and
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C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
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                                                                                                     A;Cross-references: EMBL:X55049; NID:9511039; PIDN:CAA38889.1; PID:9511040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-107 <MEE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                         Match 81.4%; Score 538; DB 2; L Local Similarity 96.2%; Pred. No. 3.2e-40; es 102; Conservative 4; Mismatches 0;
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95.3%; Pred. No. 1.6e-39;
live 4; Mismatches 1;
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   A;Status: preliminary; translation not shown
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C;Comment: The sequence shown is HP R16.7.
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C;Keywords: heterotetramer
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                                          A; Molecule type: DNA
A; Residues: 1-108 <WY3>
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S69900
Ig kappa chain (clone KL2.18 / KL4810 / KL4C11) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69900; S69907; S69908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-212, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900
A;Status: preliminary; translation not shown 'A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: BMBL:X55041; NID:g511023; PIDN:CAA38881.1; PID:g511024
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Cross-references: BMBL:X55048; NID:g511037; PIDN:CAA38888.1; PID:g511038
A;Residues: 1-108 <WYZ>
A;Residues: BMBL:X55048; NID:g511037; PIDN:CAA38888.1; PID:g511038
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S69903
IG kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69903; S69904; S69906; R.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
R;Wysocki, L.J.; Creadon, G: Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69903
A;Cession: S69903
A;Cession: S69904
A;Residues: 1-108 <Wys>
A;Cession: S69904
A;Accession: S6904
A;A
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                                                                                                             1 FQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRL 60
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A;Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A;Accession: S69905
                                                                          PQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRL
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   Gaps
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   0; Indels
3; Mismatches
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Matches 103; Conservative
109; Conservative
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A; Residues: 1-108 <WY3>
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Best Local Similarity 94.3<sup>3</sup>
Matches 100, Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                         Species: Mus musculus (house mouse)
                                                                                                                                1 DIQMTQTTSSLSASLGDRVAISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
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                                                                                                   21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
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R; Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P. submitted to the EMBL Data Library, March 1992
A; Description: Structural characterization of CD4 mAb.
A; Reference number: S19963
A; Accession: S19970
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-108 < WEI>
A; Cross-references: EMBL: X65095; NID: 955286; PIDN: CAA46223.1; PID: 97. Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology < IMM>
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R. Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 6244-6248, 1987
A.Title: Identity of the V-kappa-10-Ars-A gene segments of the A-Title: Identity of the V-kappa-10-Ars-A gene segments of the A-Accession: A28044
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology
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                      Length 107;
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Score 529; DB 2; Leng
Pred. No. 1.9e-39;
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                                                            3; Mismatches
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                    80.0%;
95.3%;
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Local Similarity 93.4%;
les 99; Conservative
                  Query Match
Best Local Similarity 95.3'
Matches 101; Conservative
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Ig kappa chain V region (anti-CD3) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH088
R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A;Atitle: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy A;Reference number: PH0885; MUID:92113462; PMID:1346155
                                                                                                                                                                                                                       sustained by interleukin
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Ig kappa chain (clone KL2.28) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Daces: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: S69902 R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C. Immunology 75, 116-1121, 1992 in the A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by A;Reference number: S69900; MUID:92165291; PMID:1537587
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Cippedies: Wis musculus (house mouse)
Cipate: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
CiAccession: S38862
Rifischer, K.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
Rubmitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;Ie-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 2.9e-39;
4; Mismatches 2; Indels
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21 DIOMIQITSSLSASLGDRVIISCRASQDISSYLMWYQQKPDGTIXLLIYYTSRLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.2%; Score 523.5; DB 2; Length 108; Best Local Similarity 93.5%; Pred. No. 5.9e-39; Matches 100; Conservative 6; Mismatches 0; Indels 1; Gaps
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A,Reference number: S37200
A,Accession: S38862
A,Status: preliminary
A,Rolecule type: mRNA
A,Residues: 1-108 <FIS>
A,Cross_references: EMBL:X75854; NID:6429109; PID:g429110
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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1 MVSSAQFLGLLLLCFQGTRC.......CQQGNTLPYTFGGGTKLEIN 127
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## ALIGNMENTS

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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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"Complete amino acid sequence of light chain variable regions derived
"Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
-!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
HSSP; P01607; IREI.
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                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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95.3%; Pred. No. 4.2e-46;
with amatches 2; Indels
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                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 01, Last annotation update)
Ilg kappa chain V-V region HP 93G7.
Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
Mus musculus (Mouse).
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MEDLINE=82150934; PubMed=6801658;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGY; 1.
PROSITE; PS50835; IG_LIKE; 1.
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               KVSL MOUSE
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                             P01645;
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Siegelman M., Capra J.D.;

"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

-!- MISCELLANBOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

INTERPRO; IPRO07110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003996; Ig_W.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMIQHTGTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 8.3e-46;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                     FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11965 MW; 39971BC653EFEFA2 CRC64;
-i- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
HSSP; P01607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-EEB-2003 (Rel. 41, Last annotation update)
1g kappa chain V-V region HP 123E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQITISSESASLGHRVIITCSASQDISNYLNWYQQKPDGTVKLLIYYTSKLHSGVPS 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                   MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to.
phenyloxazolone and its early diversification.";
Nature 304:320-324 (1983).
-!- MISCELLANBOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 RFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
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COMPLEMENTARITY-DETERMINING-2.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Rappa chain V-V region MOPC 173.
Mus musculus (Mouse).
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region NQS-89.4
                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
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BY SIMILARITY.
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SMART; SMO0406; 167; 1.
PROSTITE; PS50815; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
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SEQUENCE.
MEDLINE=76091934; PubMed=812696;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfan; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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88
97
107
88
                                                                              Mus musculus (Mouse)
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nes 95; Conserv
                                                                                                                                                                   SEQUENCE FROM N.A.
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Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype.";

L. MISCELLANGOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

- I- MISCELLANGOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

R. HSSP, PO1607; IRED.

R. InterPro; IPR007110; Ig-like.

R. InterPro; IPR003006; Ig-N.

R. Pfam; PF00047; Ig. 1.

R. SMART; SM04406; IG-V.

R. Pfam; PF00047; IG-LIKE; 1.

R. PROSITE; PS50835; IG-LIKE; 1.

M. Immunoglobulin V region.

T. DOMAIN.
                                                                                                              21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
                                                                                                                                   DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
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                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                        Length 108;
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                 78.1%; Score 516; DB 1; Length 10v
93.4%; Pred. No. 6.6e-45;
....marches 3; Indels
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91.5%; Pred. No. 1.3e-44;
ive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11961 MW; D52EDA5E9A45291C CRC64;
   108 AA; 11989 MW; 4C98599C08EBA09A CRC64;
                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-FEB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-V region HP 91A3.
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Best Local Similarity 91.5'
Matches 97; Conservative
                                                                            99; Conservative
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108 1
108 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   MOUSE
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     SEQUENCE
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ID KVSU MOU
AC P04946;
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ID KVIW HI
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MEDLINE=19221900; PubMed=111146;
Seidman J.G., Max B.E., Leder P.;
"A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.";
Nature 280:370-375(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burstein Y., Schechter I., "Amino extra piece segments of the Mamino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambdal-type and kappa-type light
            "Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the light chain."; Eur. J. Blochem. 59:525-537(1975).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=67056897; PubMed=4162931;
Gray W.R., Dreyer W.J., Hood L.;
"Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 155:465-467(1967).
-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
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                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                    FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.6%; Score 473; DB 1; Length 10:
llarity 83.0%; Pred. No. 1.3e-40;
Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11819 MW; 2AD29D92A72AA0A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01639; P01640;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region MOPC 41 precursor.
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                                                                                                                 HSSP; PO1607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; Ig_LIKE; 1.
                                                                                                                                                                                                                                                                  [mmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
Fougereau M.;
                                                                                              PIR; A01926; KVMS73.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kappa chains.";
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 MRAPAQI FGFULLLEQCTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  IG KAPPA CHAIN V-V REGION MOPC 41.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
MISSING (IN 25% OF THE MOLECULES)
SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY - DETERMINING - 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14311 MW; SEFEOFE71D5F1BEC CRC64;
                                                 PIR; A93211; KVMSM4.

HSSP; P01607; 1REI.

InterPro; IPR007110; Ig-like.

InterPro; IPR003506; Ig MHC.

InterPro; IPR0047; ig.

Pfam; PF00047; ig.

PROSITE; P850835; IG_LIKE; 1.

Immunoglobulin V region; Signal; Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.2%; Score 451; DB 1;
70.6%; Pred. No. 2.6e-38;
iive 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-3
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PIR; A01883; KIHUWK.
HSSP; P01607; 1REI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GTKLEI 128
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InterPro; IPR003596; Ig_v.
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SEQUENCE
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                                                                                                 SIGNAL
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KV11_HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=81052342; PubMed=6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma.";
Nature 287:603-607(1980).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION WALKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 129;
                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      14069 MW; F941FA07D4AFC2F9 CRC64;
GO, GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0005855; P:immune response; NAS.
InterPro; IPR007110; 19-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003586; Ig_V.
Pfam; PF00447; Igy; 1.
SMART; SMO0406; IGY; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%; Score 431; DB 1; 70.5%; Pred. No. 2.6e-36; iive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region Tl precursor.
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                                                                                                                                    SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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InterPro, IPR007110, Ig-like.
InterPro, IPR003006, Ig_MHC.
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56
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129
129 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-V REGION TI.
PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
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"Evolution of immunoglobulin V genes: evidence indicating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 62.9%; Score 416; DB 1; Length 12
Local Similarity 63.5%; Pred. No. 8.1e-35;
les 80; Conservative 20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                             | 43 | FRAMEWORK-1. |
| 54 | COMPLEMENTARITY-DETERMINING-69 |
| 76 | FRAMEWORK-2. |
| 108 | FRAMEWORK-3. |
| 117 | COMPLEMENTARITY-DETERMINING-127 |
| 18 | BY SIMILARITY. |
| 19 | BY SIMILARITY. |
| 10 | BY SIMILARITY. |
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region HK101 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA
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MEDLINE=83129397; PubMed=6402305;
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Pfam; PF00047; ig; i. "-
SMARY; SM00406; IGy. i. "-
PROSITE; PS50835; IG LIKE; i.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kappa genes and a pseudogene.";
Nature 288:730-733(1980).
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79; Conservative
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                              PIR; A91663; K1HURE.
PDB; 1REI; 17-FEB-84.
PDB; 1AR2; 12-NOV-97.
PDB; 1BWW; 29-DEC-99.
                                                                                                                                                                                                                                                                          108 AA;
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     Wmunoglobulin V
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SEQUENCE
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KV10 HUMAN
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MEDLINE=77250895; PubMed=70482;

A Capra J.D., Tung A.S., Nisonoff A.;
Structural studies on induced antibodies with defined idiotypic
T specificities. V. The complete amino acid sequence of the light chain
Variable regions of anti-p-azophenylarsonate antibodies from A/J mice
T variable regions of anti-p-azophenylarsonate antibodies from A/J mice
L J. Immunol. 119:993-999(1977).

- !- MISCELANBOUST THE MIXTURE SEQUENCED CONTAINED AT LEAST TWO OR
THREE DIFFERENT LIGHT CHAINS. PEPTIDES CONTAINING THE FOLLOWING
SUBSTITUTIONS WERE ALSO ISOLATED: 3-VAL, 10-ILE, AND 12-LEU;
C 22-LEU; 36-PHE, 41-GLU, AND 43-ALA; 63-THR AND 68-ARG; 76-SER,
T7-SER, 78-VAL, 80-ALA, AND 85-ASP; AND 100-GLN AND 107-ARG.
R HSSP; P80352; 1MTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AQLIGLLICFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKPEKAP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.3%; Score 412; DB 1; Length 117; Best Local Similarity 72.1%; Pred. No. 1.8e-34; Matches 80; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION HK10 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-V regions (Anti-arsonate antibodies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12799 MW; D7D0FF3718CEF587 CRC64;
                                                                      GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; IQ-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_VHC.
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                                                                                                                                                                                                                                        PEam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
EMBL; V00558; CAA23824.1; -. PIR; A01881; K1HU11. HSSP; P01607; 1REI.
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56
71
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Palm M., Hilschmann N.;
Palm M., Hilschmann N.;
The primary structure of a crystalline monoclonal immunoglobulin
Mappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMIQIPSSLSASLGDRVSISCRASQDLSQYLFWYQQKPGQPPKLLIYRVSRLTNGVPD
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MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman B.E., Schiffer M., Huber R., Palm W.;
The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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GO: GO: 0003823; F:antigen binding activity; NAS.
GO: GO: 0003823; F:antigen binding activity; NAS.
GO: GO: 000595; P:immune response; NAS.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fam: PF00047; ig_1 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RESGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
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COMPLEMENTARITY - DETERMINING-1.
                                                                 COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                   61.4%; Score 406; DB 1; Length 108; 74.5%; Pred. No. 6.7e-34;
                                                                                                  FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                  12056 MW; AE2861E6AAC09DD2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 6.7e-34; 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
18 Kappa chain V-I region Rel.
Homo sapiens (Human)
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BY SIMILARITY
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7 AQLIGLILIMLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKPGKAP
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                                                                                                                                                                                                                                                                                                                                                                                                              5 AQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-35.

MEDLINE-81267384; PubMed=6167731;
Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-related fragment of the human kI Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                   KAPPA CHAIN V-I REGION DAUDI.
                                                                                                                                                                                                                                                                                                                                                    60.5%; Score 400; DB 1; Length 129; 62.8%; Pred. No. 3.3e-33; Live 19; Mismatches 26; Indels
                                                                                                                                                                 IG KAPPA CHAIN V-I REGION DAUD
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
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    SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPRO0110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
FEAN; PRO0477; ig; 1.
SWART; SMO0406; ICV: 1.
R PROSITE; PS50835; IG_LIKE; 1.
R PROSITE; PS50835; IG_LIKE; 1.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-EBB-2003 (Rel. 41, Last annotation update)
1g kappa chain V-I region WAT.
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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es 76; Conserv
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127 D 127
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P80362;
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NON TER
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KV1Y_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMIQTISSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=85014148; PubMed=6091049;
MEDLINE=85014148; PubMed=6091049;
MIChoeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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   COMPLEMENTARITY-DETERMINING-1.
                 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
                                                             COMPLEMENTARITY-DETERMINING-3
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                                                                                                                                                                                                                                                                                                                                                                                                            11902 MW; 9E8143E1188BCE2A CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Daudi precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA
                                               FRAMEWORK-3.
                                                                            FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.55
Best Local 77; Conservative
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49
56
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107
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108 AA;
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1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

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Scoring table:

Searched:

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Perfect score: Seguence:

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Q8klf3 mus musculu Q8klf1 mus musculu Q8klf1 mus musculu Q9qyf0 mus musculu Q9qyf0 mus musculu Q90m37 mus musculu Q8klf2 mus musculu Q8kcd6 mus musculu Q9kcd0 mus musculu Q9tlf8 mus musculu Q9118 homo sapien Q8uls homo sapien Q9uls homo sapien Q9uls homo sapien Q9uls homo sapien Q9uls homo sapien Q9116 mus musculu Q9118 mus musculu Q9112 mus musculu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25,9 kDa protein.
Mus musculus (Mouse).
                             090YF0
099M37
08K1F2
08K0F6
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563.024 Million cell updates/sec
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                                                                     ; Search time 58.2083 Seconds
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1 MVSSAQFLGLLLCFQGTRC.......CQQGNTLPYTFGGGTKLEIN 127
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             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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                                                   OM protein - protein search, using sw model
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Q91WS9
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sp_mammal:*
sp_mhc:*
sp_phage:*
sp_plant:*
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sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 st
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sp_bacteria:*
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; 1.
Hypothetical protein.
NON TER 1 1
SEQÜENCE 233 AA; 25781 MW;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PP00047; ig; 1.
SMART; SM0406; IGv; 1.
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                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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86.8%; Score 574; DB 11; Length 234;
Best Local Similarity 87.3%; Pred. No. 5.8e-54;
Matches 110; Conservative 7; Mismatches 9; Indels
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C TISSUE-Colon;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to 1 EMBL/GenBank/DDBJ databases.
R EMBL; BC027418; J. A.H427418.1; -.
R InterPro; IPR003106; Ig-like.
R InterPro; IPR003106; Ig-like.
R InterPro; IPR003106; Ig-like.
R InterPro; IPR003106; Ig-like.
R Ffam; PP00047; Ig, 2
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS00390; IG_MHC; 1.
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TISSUB-COlon;
Straubberg R.,
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
RENUENCE 234 Aa; 25857 MW; 4EB08C81426AEAB1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25,8 kba protein (Fragment).
Mus musculus (Mouse).
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                                   121 GTKLEV 126
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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TREAIN=BALB/C;
Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,
Foon K.A., Chatterjee S.K.;
Foon K.A., Chatterjee S.K.;
Construction and characterization of a chimeric fusion protein
consisting of an anti-idiotype antibody mimicking a breast cancer-
associated antigen and the cytokine GM-CSF.";
Hybridom 18:193-202(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                         Query Match 80.8%; Score 534; DB 11; Length 233; Best Local Similarity. 87.1%; Pred. No. 1.2e-49; Aatches 101; Conservative 7; Mismatches 8; Indels Conservative 7; Mismatches 8; Indels Conservative 7; Mismatches 8; Indels Conservative 7; Mismatches 101; Conservative 7; Mismatches 101; Conservative 7; Mismatches 8; Indels Conservative 7; Mismatches 101; Mismatches 101; Mismatches 101; Mismatches 101; Mismatches 101; Mismatches 101; Mismatches 
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233 AA; 25781 MW; BIC184DA149A16EB CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last seque)
01-MAR-2003 (TrEMBLrel. 23, Last annot:
Immunoglobulin light chain (Fragment):
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Homo sapiens (Human)
                                             Query Match
Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                       is cross-reactive
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                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adderson E.B., Shikhman A.R., Ward K.B., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from
rheumatric carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes:";
J. Immunol. 161:2020-2031(1998).
                                                                                                                                                                                                                                             STRAIN=BALB/c;
MEDLINE=20448942; PubMed=10992488;
MEDLINE=20448942; PubMed=10992488;
MILiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-rewith cardiac myosin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.1%; Score 430; DB 11; Length 107; 78.3%; Pred. No. 7.9e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGXDYSLTISNLEPEDIATYYCQOYSKFPWTFGGGTKLEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 AA; 11648 MW; ACF9B1253ACA1E5D CRC64;
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EMBL, AF206022; AAF69320.1;
HSSP: P80362; IWTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGV; 1.
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PROSITE; PS50835; IG LIKE; 1.
NON TER 107 107
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                                                                                                                Mus musculus (Mouse)
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                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.0%; Score 390; DB 4; Length 108; Best Local Similarity 71.7%; Pred. No. 1.7e-34; Matches 76; Conservative 12; Mismatches 18; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                           13; Indels
107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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Last annotation update).
                                                    DB 4;
                                                    59.4%; Score 392.5; DB 4 ilarity 74.8%; Pred. No. 9.1e-35; Conservative 11; Mismatches 13
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Clin. Immunol. Immunopathol. 87:184-192(1998)
BMBL; AP035037; AAD56273.1; -.
INSEP: PO1667; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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SMART, SM00406, IGv, 1.
PROSITE, PS50835; IG_LIKE, 1.
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Homo sapiens (Human)
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les 74; Conserv
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                                                                                                                                 (Fragment)
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Matches
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Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                      Query Match 58.9%; Score 389; DB 11; Length 234; Best Local Similarity 61.2%; Pred. No. 6.1e-34; Matches 74; Conservative 19; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
                           Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; AAH19474.1; -
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig WHC.
Ffam; PF00047; Ig; 2.
SMART; SMO466; IGv.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                      al protein.
234 Aa; 25702 MW; 102551C58AC2FA9F CRC64;
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EMBL; AF035044; AAD56280.1; -.
HSSP; PO1607; IREI.
InterPro: IPR007110; Ig-like.
InterPro: IPR00396; Ig_WHC.
InterPro: IPR00396; Ig_V.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGV.
NOW.
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                                                                                                                                                                                                                                                                                                                                                                         108 AA
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Matches 76; Conservative
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108 AA;
        SEQUENCE FROM N.A.
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                     TISSUE=Colon;
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SEQUENCE 23
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SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF152171; AAD40242.1; -.
HSSP; PO1679; 2FBJ.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.1%; Score 370.5; DB 4; Length 107; 69.8%; Pred. No. 2.2e-32; ive 12; Mismatches 19; Indels 1;
61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEI 106
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                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 23, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; PO1607; IREI.
InterPro; IPR003106; Ig-NHC.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR0030596; Ig_N.
SMART; SM00406; IGV;
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NON TER.
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1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60
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                                                                                                                                                                                                                                                                    Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307935; AAL09419.1;
InterPro: IPR007110; Ig-like.
InterPro: IPR003106; Ig MiC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.9%; Score 363; DB 11; Jength 111; Best Local Similarity 63.6%; Pred. No. 1.5e-31; Matches 70; Conservative 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AA; 12046 MW; 1E46988AA6858526 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Pterin-mimicking anti-idiotope kappa chain variable
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Last annotation update)
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53.1%; Score 351; DB 11;
Best Local Similarity 60.4%; Pred. No. 2.8e-30;
Matches 64; Conservative 22; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1. SMART; SMO0406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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SMART; SM00406; IGv; 1
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                                                                                                            Mus musculus (Mouse)
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                                                                                     Fragment)
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                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLLIYYTSRLHSGVPS 80
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEI 106
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                55.5%; Score 367; DB 11; Length 2 66.0%; Pred. No. 1.3e-31; tive 17; Mismatches 19; Indels
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                                                                                                                                                                                          214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
HSSP; PO1607; IREI.
InterPro: IPR007110; Ig-like.
InterPro: IPR003506; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam; PF0047; ig; 1.
SMART; SM06406; IGv. 1.
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Q920E9;
01-DEC-2001 (TrEMBLrel. 19, Created)
                               Pfam; PF00047; ig; 2.

SMART; SM00406; IGy; 1.

PROSITE; PS50835; IG LIKE; 2.

PROSITE; PS00290; IG_MHC; 1.

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SEQUENCE 214 AA; 23322 MW;
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InterPro; IPR003596; Ig_v.
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Best Local Similarity 66.0*
...ham 70; Conservative
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Best Local Similarity 69.5-
Best A4; Conservative
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                                                       1 DIWMTQSQTFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASYPYSGVPH 60
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MEDLINE=21361171; PubMed=11468171;

A Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;

A Comerzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;

The tropism of organ involvement in primary systemic amyloidosis:

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                            52.6%; Score 348; DB 4; Length 116; 62.9%; Pred. No. 6.6e-30; ive 20; Mismatches 19; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kappa 1 light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA
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Best Local Similarity 62.9°
Matches 66, Conservative
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1096PF6
AC 096PF7
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DT 01-DB6
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Search completed: October 22, 2003, 22:20:15 Job time: 60.2083 secs

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SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
JS-08-137-117D-29
Sequence 29, Appl
Sequence 2, Appl
Sequence 2, Appli
Sequence 17, Appl
Sequence 5, Appli
Sequence 37, Appl
Sequence 37, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                        October 22, 2003, 22:14:35; Search time 13.4697 Seconds (without alignments) 398.931 Million cell updates/sec
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                                                                                                                                           1 MVSSAQFLGLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
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                                                                                                                                                                                                                                                                                                                                 /cgm2_6/ptcdata/2/iaa/5A_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-USSS-05262-2
US-08-458-05262-2
US-08-458-100-17
US-08-458-110-37
US-08-137-1170-37
US-08-574-699A-2
US-09-225-322B-10
US-09-764-304-10
US-09-764-304-19
US-09-364-19
US-09-364-19
US-08-44-19
US-08-434-372-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-437-642B-16
US-08-4458-516-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-121-054C-18
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-137-117D-29
                                                                                                                                                                                                  328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     protein - protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*
                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                     US-09-114-285A-29
661
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
128
128
128
127
127
107
107
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Perfect score:
                                                                                                                                                                 Scoring table:
                                                                                                                                            Sequence:
                                                                                                                                                                                                  Searched:
                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                                                                                        1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGBRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                              1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ROdriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: MILLOR MONOCLONAL ANTIBODIES WHICH PROMOTE
TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,520
FILING DATE: 29-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISFRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MAV92-01
TELECOMMUNICATION INFORMATION:
                                                                                            Query Match 100.0%; Score 661; DB 2; Best Local Similarity 100.0%; Pred. No. 3.8e-61; Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08236520 ; Patent No. 5591629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                           ; MOLECULE TYPE: protein US-08-436-717-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-236-520-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||
121 GTKLEIN 127
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                                                                                                                                                                                                                                                                                               61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                         1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
                                                                                                                                                                                                   1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                      .
0
                                                                                                      Length 127;
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US-08-436-717-29
is Sequence 29, Application US/08436717
is Sequence 29, Application US/08436717
is Sequence 29, Application US/08436717
is GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: DONES, Steven
APPLICANT: BALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                 Query Match 100.0%; Score 661; DB 1; Best Local Similarity 100.0%; Pred. No. 3.8e-61; Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
PILING DATE: 19-PEB-1992
PRIOR APPLICATION DATA:
FILING DATE: 19-PEB-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-PEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: WEGNET, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: (202)672-555
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                         , MOLECULE TYPE: protein US-08-137-117D-29
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTKLEIN 127
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TOPOLOGY: linear
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STATE: D.C.
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MVSSAQFLGLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                             APPLICANT: Mayor Foundation for Medical Education Research TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C. STREET: Two Milltia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.5%; Score 638; DB 5; Length 13:
96.0%; Pred. No. 9.5e-59;
ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION STATE:
ATPOINT APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: APPLICATION NUMBER: U.S. 08/236,520
FILING PATE: APPLICATION NUMBER: U.S. 08/236,520
FILING PATE: APPLICATION:
NUMBER: APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFREENCE/DOCKET NUMBER: MMV92-01 PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   Sequence 2, Application PC/TUS9505262 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08649100
Patent No. 6114507
GENERAL INFORMATION:
APPLICANT: SHIRARAWA, KAMON
APPLICANT: MATUSUB, TOWOKAZU
APPLICANT: NAGATA, SHIGEKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-861-550 C TELEFAX: 617-861-550 C SEQUENCE CHARACTERISTICS: LENGTH: 131 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.0'
                                                                                                                                                                                                                                                                                                                                       STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
2IP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-05262-2
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GTKLEI 126
                                        121 GTKLEI 126
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121
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-458-516-5
; Sequence 5, Application US/08458516
; Sequence 5, Application US/08458516
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: TSo, J. Yun
; TITLE OF INVENTION: GPIIB/IIIA
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 127;
                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
ZIP: 22040-0747
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%; Score 621; DB 3;
93.7%; Pred. No. 5.3e-57;
tive 7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: WIREHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFRENCK/COCKET NUMBER: 1110-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.7
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 127 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-649-100-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GTKLEI 126
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61 DGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIASYFCQQGYTPPWTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DGTIKLLIYYTSRLHSGVPSRFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 92.6%; Score 612; DB 1; Length 127; Best Local Similarity 92.1%; Pred. No. 4.5e-56; Matches 116; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37.3

Sequence 37.3

Sequence 37.3

Batent No. 5817790

GENERAL INFORMATION:

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: BENDIG, Mary

APPLICANT: SALOANHA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                               53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
ZIP: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0,
                           PRIOR ADDICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: J9-FEB-1992
RION APPLICATION NUMBER: JP 3-95476
FILING DATE: Z5-ARR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: Z5,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 127 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-137-117D-37
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Patent No. 5795865

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, Masayuki

APPLICANT: BENDIG, Mary

APPLICANT: ONES, Steven

APPLICANT: APPLICANT: JONES, Steven

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109.
ZIP: 20007-5109.
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 619; DB 1;
Pred. No. 8.5e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...urESSEE: ... AUURESS:
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
                                                                                                                                                             FILING DATE:
CLASSIFICATION 1424

PRIOR APPLICATION 1424

PRIOR APPLICATION 1424

PRIOR APPLICATION 1424

PRIOR APPLICATION 1426

FILING DATE: 03-MAY-1993

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-37-3

TELECHONINICATION INFORMATION:
TELECHONINICATION INFORMATION:
TELECHONINICATION INFORMATION:
TELECHONINICATION INCORMATION:
TELECHONINICATION INCORMATION 
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Best Local Similarity 92.9
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-458-516-5
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSSAQFLGLLLLCFQVTRCDIQMTQTTSSLSASLGDRVIISCRASQDISNYLSWYQQKP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641 US-09-225-3228-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                              Score 606; DB 2;
Pred. No. 1.9e-55;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 574; DB 4;
Pred. No. 3.9e-52;
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CURRENT PELING DATE: 1999-01-05
READ APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR PILING DATE: 1991-09-18
NUMBER: OF SEQ ID NOS: 19
SEQ ID NOS: 19
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                                                   REGISTRATION NUMBĒR: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09225322B
                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
90.5%;
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Best Local Similarity 86.5%;
Matches 109; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.5
Matches 114; Conservative
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-225-322B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVSTPQFLGLLLICFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 127;
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APPLICANT: MITJANS, Francesc
APPLICANT: MITJANS, Francesc
APPLICANT: MITJANS, Francesc
APPLICANT: ROSELL, Elisabet
APPLICANT: ADAN, Jaume
APPLICANT: ADAN, Jaume
APPLICANT: ADAN, Jaume
APPLICANT: ADAN, Jaume
APPLICANT: ADAN, Simon
APPLICANT: HANN, Diane
TITLE OF INVENTION: Anti-alpha-V-Integrin Monoclonal
TITLE OF INVENTION: Antibody
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 220 Clarendon Blvd.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.6%; Score 612; DB 2;
92.1%; Pred. No. 4.5e-56;
tive 7; Mismatches 3;
                                                                                                                                                                                                                                                                   53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
RIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94120165.9
FILING DATE: 20-DEC-1994
                                        APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/ABRIT INFORMATION:
NAME: WEGNET, HAROLD C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08574699A Patent No. 5985278
FILING DATE: 24-APR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.6
Best Local Similarity 92.1
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-436-717-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
COMPUTER: IBM PC COMP
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US-08-574-699A-2
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                           61 DCTVKLLIFYSSNLHSGVPSRFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MMSSAQFLGLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HANL, NUGUEL
APPLICANT: HANL, NUGUEL
APPLICANT: HANL, NUGUEL
APPLICANT: HANL, NUGUEL
APPLICANT: MIYAJI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REPRERNCE: 249-101
CURRENT FILING DATE: 1999-01-05
CURRENT FILING DATE: 1999-01-05
PRIOR FILING DATE: 1995-05-31
PRIOR FILING DATE: 1995-03-21
PRIOR PLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-03-21
PRIOR FILING DATE: 1995-09-17
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1992-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALEGRILIN VET: 2.0
SEQ ID NO 19
LENGTH: 128
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Sequence 10, Application US/09764304
Sequence 10, Application US/09764304
Setent No. 6495666
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, NAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:light chain; OTHER INFORMATION: variable region
US-09-225-3228-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.8%; Score 574; DB 4; Best Local Similarity 86.5%; Pred. No. 3.9e-52; Matches 109; Conservative 8; Mismatches 9;
                                                                                                                                                                                                                                                                   Sequence 19, Application US/09225322B
Patent No. 6437098
PERERAL INFORMATION:
APPLICANT: SHITARA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                              121 GTKLEI 126
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US-09-225-322B-19
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61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
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Sequence 19, Application US/09764304
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, MOBUO
APPLICANT: HANAI, MOBUO
APPLICANT: MINAJI, HIROWASA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT FILING DATE: 2010-10-19
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER PILING DATE: 1995-01-05
EARLIER PELING DATE: 1995-03-21
EARLIER PILING DATE: 1995-03-21
EARLIER PILING DATE: 1994-08-17
EARLIER PILING DATE: 1991-09-18
SARLIER PILING DATE: 1991-09-18
SEALIER PILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 19
LENGTH: 128
THORY HIS DATE: 108
THORY HIS DATE: 108
THORY HIS DATE: 108
THORY HIS DATE: 108
THORY HIS DATE: 1991-09-18
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CURRENT FILING DATE: 2001-01-01
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1999-01-05
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-05-31
EARLIER FILING DATE: 1995-03-21
EARLIER FILING DATE: 1995-03-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1992-09-17
EARLIER FILING DATE: 1992-09-17
EARLIER FILING DATE: 1992-09-17
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENTING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARENTING DATE: 1991-09-18
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: CDNA KM-641 US-09-764-304-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GTKLEI 126
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Length 127; Indels

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61 DGTVELLIYHTSRLQSGVPSRFSGSGSGTDYSLTISDLEQEDIATYFCQQGYTLPYTVGG 120
                                                                                                                                                                                            DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                 1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANI, No. 6538111uo
TAKATSU, Kiyoshi
TILE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 556; DB 4; Length 127; Pred. No. 2.8e-50;
                     Query Match 84.1%; Score 556; DB 3; Best Local Similarity 84.1%; Pred. No. 2.8e-50; Matches 106; Conservative 10; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IEM. Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/434,122
FILING DATE: 05-NO. 6538111-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-434-122-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09434122
Patent No. 6538111
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                             GTKLEI 126
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                 61 DGTIKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTINNLEQEDIATYFCQQGNTLPYTFGG 120
                                                                                                                                                                                                                                                     1 MMSSAQFLGLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP 60
                                                                                                                                                                                                             1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTS$LSASLGDRVTISCRASQDISSYLNWYQQKP
                                                                                                                                                                        ò
                                                                                                                          Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
TITLE OF INVENTION: Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    9; Indels
                                                                                                                          Score 574; DB 4;
Pred. No. 3.9e-52;
8; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
CLASSTERMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihira
ANAZAWA, Hideharu
HANAI, NO. 6018032uo
                     ; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08836561
Patent No. 6018032
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
APPLICANT: FURUYA, Akiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTR. 2
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                          86.8%;
86.5%;
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 amino acids
                                                                                                                                                                  Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-836-561-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                Best Local Similarity
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US-08-836-561-29
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                            Query Match
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Matches 106; Conservative 10; Mismatches 10; Indels
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121 GTKLEI 126
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Sequence 34, Appli Sequence 1, Appli Sequence 30, Appli Sequence 32, Appl Sequence 32, Appl Sequence 113, Appl Sequence 103, Appl Sequence 103, Appl Sequence 98, Appl Sequence 98, Appl Sequence 92, Appl Sequence 10, Appl Sequence 21, Appl Sequence 22, Appl Sequence 24, Appl

S US-10-310-674A-34 S US-10-114-908-7 US-09-813-659-30 US-09-813-659-30 US-09-813-659-32 US-10-207-655-348 US-10-207-655-348 US-10-207-655-348 US-10-203-349-103 US-10-203-349-98 US-10-203-349-98 US-10-203-349-98 US-10-203-349-98 US-10-203-349-92 US-10-203-349-98 US-10-203-349-92 US-09-05-6108-10 US-09-05-6108-10 US-09-29-665-21 US-09-205-24-33 US-10-110-729-71

Sequence 30, Appl Sequence 6, Appli Sequence 1, Appli Sequence 2, Appli Sequence 11, Appl Sequence 30, App

US-09-940-166A-2 US-09-811-384-11 US-09-859-053-30 US-09-940-166A-6 US-10-227-694-1

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Sequence 21, Application US/08779784

Publication No. US20020164325A1

GENERAL INFORMATION:
APPLICANT: Redriguez, Moses
APPLICANT: Miler, David J.
APPLICANT: Miler, David A. Jackson, Esq.
CORRESPONDRNCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER KEALABLE FORD

COMPUTER: IBM PC compatible

CONFUNCATION OF COMPUTER: VC DOS MS - DOS

CONFRONT APPLICATION DATA:

APPLICATION NUMBER: US 08/692,084

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/692,084

FILING DATE: 08-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/236,520

FILING DATE: 29-APR-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
07601
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Sequence 5, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 6, Appli
Sequence 2, Appli
Sequence 1, Appli
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Sequence 64, Appl
                                                                                                 October 22, 2003, 22:16:46; Search time 23.572 Seconds (without alignments) 902.237 Million cell updates/sec
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Sequence 19, R
Sequence 10, R
Sequence 19, R
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1 MVSSAQFLGLLLLCFQGTRC......CQQGNTLPYTFGGGTKLEIN 127
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUBL_pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_NBW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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2 US-10-010-729-64
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5 US-10-265-713-10
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 5, Application US/1026883

Sequence 5, Application US/1026883

Publication No. US2030138862A1

GENERAL INPORMATION:
APPLICANT: Green, Jennifer Macphate
TILE REFERENCE: 05802.0062.NPUS01

CURRENT APPLICATION NUMBER: US/10/268,883

CURRENT FILING DATE: 2003-03-26

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-11-21

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Version 3.1

SOFTWARE: Patentin Version 3.1
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APPLICANT: YATOMI, Takehiro
APPLICANT: YATOMI, Takehiro
APPLICANT: SUDA, Takashi
TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT
FILE REFERENCE: 1110-0307P
CURRENT APPLICATION NUMBER: US/10/084,139
CURRENT FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 626; DB 12;
Pred. No. 1.9e-50;
7; Mismatches 1;
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ilarity 93.7%; Pred. No. 5.4e-50;
Conservative .7; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.78;
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Best Local Similarity 93.7<sup>1</sup>
Matches 118; Conservative
                                                    121 GTKLEI 126
                      121 GTKLEI 126
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Best Local Similarity
Matches 118; Conserv
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Publication No. US20030185827A1

GENERAL INFORMATION:

APPLICANT: Miller, David J.

APPLICANT: Miller, David J.

TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System

FILE REPRENCE: 1199-1-005CIP2

CURRENT APPLICATION NUMBER: US/10/010,729

CURRENT PELLOS DATE: 2000-11-13

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 1200-120-105

PRIOR PELLON NUMBER: 08/779,784

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1996-08-08

PRIOR PRIOR PRIOR DATE: 1996-08-08

PRIOR FILING DATE: 1996-08-08

PRIOR FILING DATE: 1996-08-08

PRIOR FILING DATE: 1999-06-29

NUMBER OF SEO ID NOS: 80

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 64
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                                                                                                                                                                                                                     Score 638; DB 8; Length 13.
Pred. No. 1.5e-51;
...antrhes 0; Indels
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96.0%; Pred. No. 1.5e-51;
cive 5; Mismatches 0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.0%;
Matches 121; Conservative
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Best Local Similarity 96.0
Matches 121, Conservative
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ORGANISM: Mus musculus
US-10-010-729-64
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US-10-010-729-64
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TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
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ORGANISM: Artificial Sequence
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GRENEAL INCOMALION:
GRENEAL INCOMALION:
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: MITADA GRAWA, WAMORU
APPLICANT: MITADA GROESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT PILING DATE: 2001-01-19
CURRENT PILING DATE: 1999-01-05
EARLIER PILING DATE: 1999-01-05
EARLIER PILING DATE: 1999-01-05
EARLIER PILING DATE: 1995-05-31
EARLIER PILING DATE: 1995-05-31
EARLIER PILING DATE: 1995-05-31
EARLIER PILING DATE: 1995-09-17
EARLIER PILING DATE: 1994-08-17
EARLIER PILING DATE: 1992-09-17
EARLIER PILING DATE: 1991-09-18
SARLIER APPLICATION NUMBER: US 08/292,178
EARLIER PILING DATE: 1991-09-18
SARLIER PILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOYEY: 2.0
SEQ ID NO 10

LENGTH: 128

WANNER OF SEQ ID NOS: 19
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Patent No. US20020026036A1
GENERAL INFORMATION: KENYA
APPLICANT: HANNI, NOBUO
APPLICANT: HASCAWA, MAMORU
APPLICANT: MIXAJI, HIROMASA
APPLICANT: KUWANA, YOSHIHISA
                                                                                                                                                                                                                                                                      Sequence 10, Application US/09764304
Patent No. US20020026036Al
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US-09-764-304-10
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Sequence 10. Application US/10166626

| Sequence 10. Application US/10166626
| Publication No. US20030166876A1
| GENERAL INFORMATION:
| APPLICANT: SHIRARA, KENYA
| APPLICANT: HANAI, NOBUO
| APPLICANT: HASEGAWA, MAMORU
| APPLICANT: MIVANI, YOSHIHISA
| TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
| FILE REFERENCE: 249-101
| CURRENT REPERINCE: 249-101
| CURRENT PELLING DATE: 199-06-12
| PRIOR PELLING DATE: 1995-06-31
| PRIOR FILING DATE: 1995-05-31
| PRIOR FILING DATE: 1995-03-21
| PRIOR FILING DATE: 1995-09-17
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CURRENT APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 2001-01-9
EARLIER APPLICATION NUMBER: US/09/764,304
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/45,680
EARLIER APPLICATION NUMBER: US 08/45,680
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-1
EARLIER FILING DATE: 1995-03-1
EARLIER FILING DATE: 1994-08-17
EARLIER FILING DATE: 1991-09-18
NUMBER: US 08/292,178
EARLIER FILING DATE: 1991-09-18
NUMBER: OF SEQ ID NOS: 19
SEQ ID NO 19
LENGTH: 128
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121 GTKLEI 126
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121 GTKLEI
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Sequence 19, Application US/10166626

Publication No. US20030166876A1

GENERAL INFORMATION:

APPLICANT: SHITARA, NOBUO

APPLICANT: HASEGAWA, MAMORU

APPLICANT: HASEGAWA, MAMORU

APPLICANT: MIYAJI, HIROMASA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101

CURRENT APPLICATION NUMBER: US/10/166,626

CURRENT FILING DATE: 1999-01-06

PRIOR FILING DATE: 1999-01-06

PRIOR FILING DATE: 1999-01-06

PRIOR PPLICATION NUMBER: US 08/408,133

PRIOR FILING DATE: 1995-03-21

PRIOR PLICATION NUMBER: US 08/408,133

PRIOR FILING DATE: 1994-08-17

PRIOR PLING DATE: 1994-08-17

PRIOR PLING DATE: 1994-08-17

PRIOR PLING DATE: 1991-09-18

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 19

LENGTH: DATE

LENGTH: 128

THENDER PATENTING DATE: 1991-09-18

SOFTWARE: PATENTING NOS: 19
                                                                                                                                                                                                                      1 MVSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCRASQDISSYLNWYQQKP
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                                                           , OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10
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                                                                                                                                       Score 574; DB 12;
Pred. No. 1.2e-45;
8; Mismatches 9;
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86.8%; Score 574; DB 12;
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9;
                                  ORGANISM: Artificial Sequence
                                                                                                                                       Query Match
Best Local Similarity 86.5%;
Matches 109; Conservative
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CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR PAPLICATION NUMBER: US/09/225,322
PRIOR PELING DATE: 1999-01-05
PRIOR PILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR PILING DATE: 1995-03-1
PRIOR PILING DATE: 1994-08-17
PRIOR PILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US 07/947,674
PRIOR PILING DATE: 1991-09-17
PRIOR APPLICATION NUMBER: US 07/947,674
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR APPLICATION NUMBER: US 07/947,674
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR PILING DATE: 1991-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MMSSAQFLGLLLCFQGTRCDIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKP
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APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, HIROMASA
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANAI, VOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
PRIOR APPLICATION NUMBER: US/09/225,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641 US-10-265-713-10
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Sequence 10, Application US/10265713; Publication No. US20030095964A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 19, Application US/10265713; Publication No. US20030095964A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                           APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 128
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61 DGTVELLIYHTSRLQSGVPSRFSGSGSGTDYSLTISDLEQEDIATYFCQQGYTLPYTVGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                       NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-86-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10140555
Publication No. US20020127227A1
GENERAL INPORMATION:
APPLICANT: Julie A. Abrahamson
APPLICANT: Stephen D. Holmes
APPLICANT: Jeffrey R. Jackson
TITLE OF INVENTION: RHAMM Antagonist Antibodies
FILE REFERENCE: P50857
CURRENT APPLICATION NUMBER: US/10/140,555
CURRENT FILING DATE: 2002-05-07
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.1%; Score 556; DB 15;
84.1%; Pred. No. 5.3e-44;
tive 10; Mismatches 10;
         APPLICATION NUMBER: JP 232384/95
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                FILING DATE: 11-SEP-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.1%
Matches 106; Conservative
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US-10-140-555-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DGTVKLLIFYSSNLHSGVPSRFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence:light chain , OTHER INFORMATION: variable region US-10-265-713-19
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PURUYA, KAZUYASU
IIDA, AKIHITO
ANAZAWA, HIGGHOSO 1020030096977Aluo
HANAI, No. US20030096977Aluo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
RECEPTOR Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 86.8%; Score 574; DB 15; Length 1
Best Local Similarity 86.5%; Pred. No. 1.2e-45;
Matches 109; Conservative 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PARCHIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/10283349 Publication No. US20030096977A1 GENERAL INFORMATION: APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                              LENGTH: 128
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Search completed: October 22, 2003, 22:21:45 Job time : 24.572 secs
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| Publication No. US20030096285A1
| Publication No. US20030096285A1
| Publication No. US20030096285A1
| APPLICANT: Tso, Jonniffer
| TITLE OF INVENTION: ANTI-HLA-DR ANTIBODIES AND THE METHODS OF USE THEREOF
| FILE REFERENCE: 05682.0062.NUUS01
| CURRENT APPLICATION NUMBER: US/10/269,010
| PRIOR FILING DATE: 2001-10-10
| PRIOR FILING DATE: 2001-10-11
| PRIOR FILING DATE: 2001-11-21
| NUMBER OF SEQ ID NOS: 2
| NUMBER OF SEQ ID NOS: 2
| CONTRACT OF THE NOS: 3
| CONTRACT OF THE NOS: 4
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                                                                                                                                                  APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NeUS011
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR PLING DATE: 2001-010
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
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Pred. No. 2.6e-41;
6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.6%; Score 526; DB 12; 93.4%; Pred. No. 2.6e-41; iive 6; Mismatches 1;
                                     Sequence 6, Application US/10268883
Publication No. US20030138862A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 107
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Best Local Similarity 93.4%;
Matches 99; Conservative
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Best Local Similarity 93.4*
Matches 99; Conservative
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US-10-268-883-6
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ORGANISM: Mouse
US-10-268-883-6
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Sequence 1, Application US/09480236;
Sequence 1, Application US/09480236;
Patent No. US20020142000A1
GENERAL INFORMATION:
APPLICANT: Digan, Mary Ellen
APPLICANT: Lake, Philip
TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
FILE REFERENCE: CGC 4-31157A/USN
CURRENT APPLICATION NUMBER: US/09/480,236
CURRENT FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SSCTAMARE: Patentin Ver. 2.0
SSCTAMARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: ScFv(UCHT-1)-PE38 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Matches 99, Conserv
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